

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:39:20 ; Search time 42 Seconds
(without alignments)
1356.198 Million cell updates/sec

Title: US-09-724-254A-3
Perfect score: 3124
Sequence: 1 MLNWVLLVLPVSGQFART.....AEFSLTHSKMLFALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	418.5	13.4	344	A41357	Fc gamma (IgG) rec
2	418.5	13.4	374	A39878	Fc gamma (IgG) rec
3	402.5	12.9	404	A46480	Fc gamma (IgG) rec
4	396	12.7	336	I48471	Fc gamma (IgG) rec
5	326.5	10.5	296	I46021	Fc gamma (IgG) rec
6	319	10.2	270	A34636	Fc-gamma receptor
7	299.5	9.6	4391	A38096	perlecan precursor
8	292.5	9.4	254	JL0107	Fc gamma (IgG) rec
9	292	9.3	233	JU0284	Fc gamma (IgG) rec
10	290	9.3	323	S06946	Fc gamma (IgG) rec
11	289	9.3	310	JL0119	Fc gamma (IgG) rec
12	275	8.8	7962	I38346	elastic titin - hu
13	272	8.7	255	JC7593	SH2 domain-contain
14	267	8.5	257	S00682	IGF Fc receptor al
15	264.5	8.5	317	JL0118	Fc gamma (IgG) rec
16	262	8.4	285	S36903	Fc gamma (IgG) rec
17	258	8.3	3707	S18252	heparan sulfate pr
18	257	8.2	261	S29360	Fc gamma (IgG) rec
19	256	8.2	280	I55577	Fc gamma (IgG) rec
20	253.5	8.1	293	1 FCN5G1	Fc gamma (IgG) rec
21	253.5	8.1	330	A40071	Fc gamma (IgG) rec
22	249.60	8.1	330	I49660	Fc gamma (IgG) rec
23	252.5	8.1	1256	T03096	CDO protein - rat
24	248.5	8.0	738	A40096	platelet-endotheli
25	244	7.8	267	I56110	Fc-gamma RIIB-alp
26	241	7.7	1694	S50065	sialoadhesin - mou
27	241	7.7	1896	T08951	Down syndrome cell
28	240	7.7	862	I49583	differentiation an
29	235.5	7.5	1240	T03097	CDO protein - huma

CD22 homolog/B lym
carcinoembryonic a
BIG-I protein - ra
Fc gamma (IgG) rec
B-cell adhesion pr
immunoglobulin-lik
axonal glycoprotei
IgE receptor alpha
connectin 3B - chi
connectin/titin -
axonin 1 precursor
hypothetical prote
hemiscitin precurs
cell adhesion prot
hypothetical prote
plasmacytoma-assoc

ALIGNMENTS

RESULT 1

A41357
Fc gamma (IgG) receptor I (high affinity) form b - human
N;Alternate names: CD64
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41357; S03019
R;Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary
A;Reference number: A41357; MUID:89100284; PMID:2911749
A;Accession: A41357
A;Molecule type: mRNA
A;Residues: 1-344 <ALL1>
A;Cross-references: UNIPROT:P12314; GB:X14355; GB:M21090; NID:G31333; PIDN:CAA32536.1; I
R;Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (Fc
A;Reference number: S03018; MUID:89098339; PMID:2974947
A;Accession: S03019
A;Molecule type: mRNA
A;Residues: 1-344 <ALL2>
A;Cross-references: ENBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334
A;Note: the authors translated the codon ACT for residue 25 as Ala
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F;117-170/Domain: immunoglobulin homology <IMM>

Query Match 13.4%; Score 418.5; DB 2; Length 344;
Best Local Similarity 37.0%; Pred. No. 8.2e-21;
Matches 108; Conservative 41; Mismatches 122; Indels 21; Gaps 10;

QY 1 MLNWVLLVLPVSGQFARTPRPIIFLOPPWTTFQGERVTLTKGFRFYSPOKTKYHR 60

Db 7 LLLMW-----FVDDQ-VDTTKAVITLQPPVSVFQEEVTLRCEVHLHPGSSSTQWFLN 59

QY 61 YLKGKILRETPD---NILEVQESGEYRCQAGSFLSPVHLDFSSASLILQAPLSVF-EG 116

Db 60 --GTATQTSTPSYRITSASVNDSGEYRCQGLSGRSDPIQLQETHRGWLLQLQVSRVFTEG 117

QY 117 DSVVLRCGA-XAEVTLNNTIYKNDVLAFLNKRDTDFHPLACLDKNGAYRCTGYKSSCCP 175

Db 118 SPLAURCHAWKDKLVYVNLVYRNGKAFKFFHWSNLTKTNISHNGTHYCSGNGKH--R 175

QY 176 VSNNTVKIQVQEPPTPRPVLRASSFQ-PSGNPVLTCTCTQLSLERSDVLPRPFRDDQT 234

Db 176 YTSAGISVTYKELFPAPVLNASVTSPLLEGNLVLTSCETKLLQRPGLQLYFYSFGSKT 235

QY 235 LGLGWSLSPNQTITAMWSKDSGFYWCXKAATMPHSVSDSPRSWTQV---QIP 283

Db 236 L-RGNTSSEYQILFARREDSGLYWCXAATEDGNVLRSPFELQVLGLQLP 286

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Db      60  --GTATGTSTPSTRAITSASVNDGSEYRCQGLSGRSDPTQLEIHRGWLLLLQVSGSRVFTG 117
Qy      117  DSVVLRCA- KAEVTLNNTIYKNDNLAFUNKRTDFHPIHACLKNDGAYRCTGYKESCCP 175
Db      118  EPLALRCHAMKDLVYNLVYRNGKAFKPFHNNSLTILKTNISHNGTYHCSGWGKH- R 175
Qy      176  VSSNTYKIQVOEPTPRVLRASSFQP- ISGNPVTLTCTQLSLERSDVPLRFRFDDQT 234
Db      176  YTSAGISVTVKELFTFPAPVLNASVTSPLLEGNLVLTSCETKLLQRFGLQYFSFYNGSKT 235
Qy      235  LGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSVTSIDSPRSWIQV---QIP 283
Db      236  L-RGRNTSSEYQILTRARREDSGLYCEAATEDGNVLKRSPELEQLVGLQLP 286

RESULT 3
A46480
Fc gamma (IgG) receptor high affinity - mouse
N;Alternate names: high affinity IgG receptor
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46480; A43511
R;Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J. Immunol. 148, 1570-1575, 1992
A;Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A;Reference number: A46480; MUID:92166399; PMID:1531670
A;Accession: A46480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <OSM>
A;Cross-references: UNIPROT:P26151
A;Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC
R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A;Reference number: A43511; MUID:9011035; PMID:2136886
A;Accession: A43511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-404 <SEA>
A;Cross-references: GB:M31314; MID:g200752; PIDN:AAA40056.1; PID:g200753
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match      12.9%; Score 402.5; DB 2; Length 404;
Best Local Similarity 36.3%; Pred. No. 1.2e-19;
Matches 107; Conservative 42; Mismatches 131; Indels 15; Gaps 10;

Qy      3  LMVI--LIVLAPVSGQFARTPRPIFLQPPMTTVQGERVTLTCKGFRFYSPQRTKWYHR 60
Db      10  MWLLTLLLVPGVGVEVYNATKAVITLQPPVWVSIPQENVTILWCPEGHPLPGDSSQTQWFIN 69
Qy      61  YLGEKILARETDNII--EVQESGYRCQAQGSPLSSPVHLDFSSASILLQAPLSVF-EG 116
Db      70  --GTAVQISTFSYSIPESAFQDSGEYRCIQIGSSMPSPVQLQIHNWLLQLQASRVLTG 127
Qy      117  DSVVLRCA- KAEVTLNNTIYKNDNLVLAFLNKRITDFHPIHACLKNDGAYRCTGYKESCCP 175
Db      128  EPLALRCHGWKNKLIVYNVYVRNGSKFQF-SSDSEVALIKTNLSHSGIYHCSGTGRH- R 184
Qy      176  VSSNTYKIQVOEPTPRVLRASSFQPI- SGNPVTLTCTQLSLERSDVPLRFRFDDQT 234
Db      185  YTSAGISVTVKELFTTTPVLRASVSPPPEGSLVTLNCTNLLQRFGLQYFSFYNGSKI 244
Qy      235  LGLGWSLSPNFQITAMWSKDSGFYWCKAATMPHSVTSIDSPRSWIQVQIP- ASHPV 288
Db      245  LEYR-NTSSEVHIAREREDAGFYWCVEATEDSSVLKRSPELEQLVGPQSSAFV 298

Fc gamma (IgG) receptor high affinity - mouse
RESULT 4
I48471

```

C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
 C;Accession: I48471
 R;Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
 Science 260, 695-698, 1993
 A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
 A;Reference number: I48471; MUID:93242399; PMID:8480181
 A;Accession: I48471
 A;Status: preliminary;
 A;Molecule type: mRNA
 A;Residues: 1-336 <RES>
 A;Cross-references: EMBL:X70980; NID:G311748; PIDN:CAA50311.1; PID:G311749
 C;Superfamily: Fc gamma receptor I; immunoglobulin homology
 C;Keywords: immunoglobulin receptor
 F;128-180/Domain: immunoglobulin homology <IMM>

Query Match 12.7%; Score 396; DB 2; Length 336;
 Best Local Similarity 36.1%; Pred. No. 2.6e-19;
 Matches 108; Conservative 43; Mismatches 130; Indels 18; Gaps 12;
 Qy 3 LWWI--LLVLAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQTKVHR 60
 Db 10 MLLTLLLLWVPVGEVGNATKAVITLQPPWASIFQKENVTLWCSPHLPGDSSTQWFIN 69
 Qy 61 YLKEILRETPD---NILEQSEGEYRCQAQSPSSPVHLDFFSSA-LILQAPLSVP-E 115
 Db 70 --GTWQTSPTSYISVASFQDSGEYRCQIGSSVPSDPVQLQIHKEDWLLQLQASRRVLTE 127
 Qy 116 GDSVILRCRA-KAEVTLNNTIYKQNVLAFLNKRTPDFHACLDKNGAYRCTG---YKE 171
 Db 128 GEPLALRCHGKRNKLVNVVFRNGSKFRP-SGGKIALKTNLSHSIYHCSNGRHYR 186
 Qy 172 SCCPVSSNTVKIQVQFPTRPVLRASSFOPI-SGNPVTILTCETQSLERSDVFRFRFR 230
 Db 187 TSAGVSI-TVKAPFLELFTTPVLRASSVSPFEGSLVTLNCTELLQRPGLQLYFSYV 245
 Qy 231 DDQTLGLWLSLNFQITAMWSDQFYWCKATMPHSVISDPSRWTVQVQIP-ASHPV 288
 Db 246 GSKILEYR-NTSEYHIAEREDAGFYWCEVATEDSSVLKHSPLKLEQLVGPSSAPV 303

RESULT 5

I46021
 Fc-gamma receptor II - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C;Accession: I46021; S40204
 R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
 Immunogenetics 39, 423-427, 1994
 A;Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.
 A;Reference number: I46021; MUID:94245284; PMID:8188320
 A;Accession: I46021
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-296 <ZHA>
 A;Cross-references: UNIPROT:Q28110; EMBL:X75671; NID:G437978; PIDN:CAA53367.1; PID:G4379
 C;Superfamily: Fc gamma receptor III; immunoglobulin homology
 C;Keywords: immunoglobulin receptor

Query Match 10.5%; Score 326.5; DB 2; Length 296;
 Best Local Similarity 37.0%; Pred. No. 1e-14;
 Matches 90; Conservative 34; Mismatches 100; Indels 19; Gaps 10;
 Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQTKVHR 60
 Db 28 MLLWTALLFLAPVSGK-PDLPRAVVTIQAWINVLREDHVTILTCGTSFSGNLTWPHN 86
 Qy 61 YLKEILRETPD---NILEQSEGEYRCQAQSPSSPVHLDFFSSA-LILQAPLSVP-EG 116
 Db 87 --GSSHTQKQPSYFRAGNSGYSRCQREQTSLSDPVHLDVSDWLLQTLPSLVQEG 144
 Qy 117 DSVVLRCRAKAEVTLNNTIYKQNVLAFLNKRTPDFHACLDKNGAYRCTGYSKESCCP 175

Db 145 EPIMLRCHSWRNQPLNKITFYQDRKSKIFSYQRTNFSIPRANLHSGQYHCTAFIGKMLH 204
 Qy 176 VGSNTVKIQVQFPTRPVLRASSFOPIGPNVTLT-TCETQSLERSDVPLRFRFRDDQT 234
 Db 205 --SSQPNVITVQE-----SSSGFSSWTAIVAGTCFAAAVAIAIITW-FRLRRRPIS 254
 Qy 235 LGL 237
 Db 255 AGL 257
 RESULT 6
 A34536
 Fc-gamma receptor II precursor - guinea pig
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
 C;Accession: A34536
 R;Tomimaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K.
 Biochem. Biophys. Res. Commun. 168, 683-689, 1990
 A;Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (I
 A;Reference number: A34536; MUID:90241239; PMID:1692213
 A;Accession: A34536
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-270 <TOM>
 A;Cross-references: GB:M35272
 C;Superfamily: Fc gamma receptor III; immunoglobulin homology
 C;Keywords: immunoglobulin receptor
 F;37-88/Domain: immunoglobulin homology <IMM>

Query Match 10.2%; Score 319; DB 2; Length 270;
 Best Local Similarity 35.6%; Pred. No. 2.9e-14;
 Matches 84; Conservative 28; Mismatches 72; Indels 52; Gaps 8;
 Qy 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPQTKVHR 60
 Db 1 MLLWTVFLAPVAGTSADPPKAVVLEPPWIVQVLRGRVTLTCGAPSPGNHSTQWLNH 60
 Qy 61 YLKEILRETPD---NILEQSEGEYRCQAQSPSSPVHLDFFSSA-LILQAPLSV 113
 Db 61 --GRLI---PTQVLPSYRFTAKGNDGSEYRCQAGTSLSDPVRLDVLSDWLVLTQSLI 114
 Qy 114 F-EGDSVILRCRAKAEVTLNNTIYKQNVLAFLNKRTPDFHACLDKNGAYRC 166
 Db 115 FQEGDIVILRCH---SWNNWPLAKVTFYHNGVAKYFSISKNFSPDQAHSHSGAYNC 169
 Qy 167 TGYKESCCPVSSNTVKIQVQFPTRPVLRASSFOPIGPNVTLTCKGFRFYSPQTKVHR 222
 Db 170 TGL-----IGRTSHTSP-----PVTITVQGPKSDSSMV 198

RESULT 7

A38096
 perlecan precursor - human
 N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prot
 C;Species: Homo sapiens (man)
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004
 C;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
 R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
 J. Biol. Chem. 267, 8544-8557, 1992
 A;Title: Primary structure of the human heparan sulfate proteoglycan from basement memb
 tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
 A;Reference number: A38096; MUID:92235084; PMID:1569102
 A;Accession: A38096
 A;Molecule type: mRNA
 A;Residues: 1-4391 <MUR>
 A;Cross-references: UNIPROT:P98160; GB:M85289; NID:G184426; PIDN:AAA52700.1; PID:G18442

R;Kallunki, P.; Tryggvason, K.
 J. Cell Biol. 116, 559-571, 1992
 A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pr
 cell adhesion molecules, and epidermal growth factor.
 A;Reference number: A41736; MUID:92112994; PMID:1730768
 A;Accession: S19256

A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phospho-
A;Reference number: A32933; MUID:89296947; PMID:2525780
A;Accession: A32933
A;Molecule type: mRNA
A;Residues: 31-254 <SCA>
A;Cross-references: GB:M24853; NID:g184849; PIDN:AAA53506.1; PID:g386806
R;Gessner, J.E.; Grussemeijer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37627
A;Molecule type: DNA
A;Residues: 1-39 <RES>
A;Cross-references: EMBL:Z46222; NID:g559445; PIDN:CAA86295.1; PID:g1478198
A;Note: translation has been corrected relative to PID:g871305
C;Comment: This low affinity Igg Fc receptor of natural killer cells, which is the produ
e nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in
C;Genetics:
A;Gene: GDB:FCGR3A; FCGR3
A;Cross-references: GDB:1119904; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: glycoprotein; receptor; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-254/Product: Fc gamma (Igg) receptor III-A #status experimental <MAT>
F;18-208/Domain: extracellular #status predicted <EXT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;111-174/Domain: immunoglobulin homology <IMM2>
F;209-229/Domain: transmembrane #status predicted <TRZ>
F;230-254/Domain: intracellular #status predicted <CYT>
F;56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 292.5; DB 1; Length 254;
Best Local Similarity 33.1%; Pred. No. 1.6e-12;
Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

Qy 1 MLLVLLVLLVAPVSGGFARTPRPIIFLOPPWTTVFGGERVLTCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVSGAGMETEDLPKAVVLEPQWVRVLEKDSVTLKCGQ--AYSPEDNSTQWF 61
Qy 59 HRYLKEILRETPDNIL----EVOESGEYRCQAQGSPLSSPVHLDFSSASIILOAPLSVF 114
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRVF 118
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRITDFHIPHACLKNDGAYRGTGYKES 172
Db 119 KEEDPIHLRCHSWKNTALHKVTLQNGKGRKYFHNSDFIYPKATLKDSGSGYFCRGLFGS 178
Qy 173 CCPVSNNTVKIQVEPFTPRVLRASSFQPIGPNVTLTCTOLSLERSDVPLRFFRDD 232
Db 179 -KNVSSETVNIITQGLA--VSTISSFFP-PCYQVSF-CLNVLLFAVDT----- 223
Qy 233 QTLGLQWSLSPNQITAMMSKSGGFYWK 261
Db 224 --GLYFSVKTNRISRTDWDKDKPKWRX 249

RESULT 9
JU0284
Fc gamma (Igg) receptor III-B precursor (neutrophil) - human
N;Alternate names: Fcr III; Igg Fc receptor precursor, type III-1 (polymorphonuclear gra
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: JU0284; S00758; I37628; B32933; A31460
R;Ravetch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A;Reference number: JU0107; MUID:89328225; PMID:2526846
A;Accession: JU0284
A;Molecule type: mRNA
A;Residues: 1-201,'Sf',204-233 <RAV>

A;Cross-references: UNIPROT:O75015; GB:J04162
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, d
rboxyl end
R;Simmons, D.; Seed, B.
Nature 333, 568-570, 1988
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membra
A;Reference number: S00758; MUID:88232937; PMID:2967436
A;Accession: S00758
A;Molecule type: mRNA
A;Residues: 1-233 <SIM>
A;Cross-references: EMBL:X07934; NID:g29744; PIDN:CAA30758.1; PID:g29745
R;Gessner, J.E.; Grussemeijer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37628
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: EMBL:Z46223; NID:g559446; PIDN:CAA86296.1; PID:g871306
R;Scallion, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phos
A;Reference number: A32933; MUID:89296947; PMID:2525780
A;Accession: B32933
A;Molecule type: mRNA
A;Residues: 1-121,'E',123-150,'S',152-233 <SCA>
A;Cross-references: GB:M24854; NID:g184851; PIDN:AAA53507.1; PID:g306930
R;Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A;Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal
A;Reference number: A31460; MUID:89128838; PMID:2521732
A;Accession: A31460
A;Molecule type: mRNA
A;Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>
A;Cross-references: GB:J04162; NID:g183036; PIDN:AAA35881.1; PID:g183037
C;Comment: This low affinity Igg Fc receptor of neutrophils, which is the product of th
l, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod
C;Genetics:
A;Gene: GDB:FCGR3B; FCGR3
A;Cross-references: GDB:128176; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linka
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-203/Product: Fc gamma (Igg) receptor III-B #status predicted <MAT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;111-174/Domain: immunoglobulin homology <IMM2>
F;56,63,82,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature for

Query Match 9.3%; Score 292; DB 1; Length 233;
Best Local Similarity 35.5%; Pred. No. 1.6e-12;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

Qy 1 MLLVLLVLLVAPVSGGFARTPRPIIFLOPPWTTVFGGERVLTCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVSGAGMETEDLPKAVVLEPQWVRVLEKDSVTLKCGQ--AYSPEDNSTQWF 61
Qy 59 HRYLKEILRETPDNIL----EVOESGEYRCQAQGSPLSSPVHLDFSSASIILOAPLSVF 114
Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRVF 118
Qy 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRITDFHIPHACLKNDGAYRGTGYKES 172
Db 119 KEEDPIHLRCHSWKNTALHKVTLQNGKGRKYFHNSDFIYPKATLKDSGSGYFCRGLVGS 178
Qy 173 CCPVSNNTVKIQVEPFTPRVLRASSFQPIGPNVTLTCTOLSLERSDVPLR 226
Db 179 -KNVSSETVNIITQGLA--VSTISSFFP-PCYQVSF-CLNVLLFAVDITGLYF 227

Best Local Similarity 25.0%; Pred. No. 2e-09;
Matches 150; Conservative 71; Mismatches 262; Indels 116; Gaps 27;

QY 23 PIIFLOPPTTTPQGRVTLTC-----KGRFVSPQTKYHYRLOKEILRE 69
DB 216 PTFSLRPKLTTFVGAARFICTVTGTPVETIWKDGAALSPSPNWRISDAENKHILEL 275
QY 70 TPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLIL-----QAPLSVFEGDSVV 120
DB 276 SN---LTIQDRGVYSCKA-----SNKFGADICQAEILLIDKPHFIKELEPVQSAINKKVH 327
QY 121 LRCA-----KAETVLTNTYK-----NDNVLAFLNKRTHFPHACLKONGAYRCTGYKES 172
DB 328 LECQVDEDRKVTWTGKQCKLPQPKDYKICFEDXIATLEPLAKLKDSGTGYVCTAGNEA 387
QY 173 CCPVSSNTVKIOVQEBFTFPVLRASSFQISGNPVTLCETQLSLERSDVPLRRFRFRDD 232
DB 388 GSSCCSACVTVREPPFVKKV---DBSYLMPLGESARLHCK---LKGSPV-IQVTFWKN 440
QY 233 QTIGLGNLSNPF-----QTAMWSKDSGYWKAATMPHSVILSDSPRSWIOVQIPAS 285
DB 441 KELSENTVRYMVFVNSEAILDITDKVEDSGSYSCAV---NDVGSDCSCTEIVIKPPS 497
QY 286 HPVLTLSPEKALNFEQTKVTLHCET-----QEDSLRT---LYRFVHEGVPLRHK 331
DB 498 F-IKILEPADIV---RGTNALLQCEVSGTGPFEISWFKQKQIRSKKYRLFSQ-----K 548
QY 332 SVRCERGAISLSLTENSGNYCTADNGLGAKPKSVLSVTVVSHVNLNLSPBDLI 391
DB 549 SLVCLSE---LFSFNSADYGEYCVVANEVGRGCGMATHL-----LKBPPTFVKKVDLI 599
QY 392 FEGAKVTLHCEAQRGSLPIL-----YQPHHEDAALERSANSAGGVAISF---SLTAHS 443
DB 600 ALGGQVTLQAAVSGSEPSISVTWKGQVIREGDKIKSPFN---GVAVLIPDVQISFG 656
QY 444 GNYCTADNGFGPQSKAVSLISITVPVSHVTLSSAAL-TFEGATVTLHCRVQSGSP 502
DB 657 GRYTCLAENAGSQTSGELI-----VKPEAKIIEAELIQTAGDPATLEYTV-AGTPE 710
QY 503 ILVCFVHEMPLVSSSTPSVGRVSF-----SFLSTEGH-SGNVCTADNGFGPQSRSE 553
DB 711 LKPKWYKDRPLVASKK---YRISFNVAQKLFYSALHDSGGQVTFEISNEVGSSCE 766

RESULT 13
JC7593
SH2 domain-containing phosphatase anchor protein 1a - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7593
A:Molecule type: mRNA
A:Residues: 1-255 <XUA>
A:Cross-references: UNIPROT:Q9BZ16; GB:AF19438
C:Genetics:
A:Gene: spapia
A:Map position: 1q21
A:Introns: 135/1; 174/1; 183/2; 212/1; 234/1; 243/3
C:Keywords: glycoprotein
F:27-135/Domain: extracellular #status predicted <EXT>
F:68-115/Domain: immunoglobulin-like #status predicted <IGL>
F:148-169/Domain: transmembrane region #status predicted <TM>
F:195-255/Domain: intracellular #status predicted <INT>

Query Match 8.7%; Score 272; DB 2; Length 255;
Best Local Similarity 57.6%; Pred. No. 3.8e-11;
Matches 57; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 371 LSVTVPSVPLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDDAALERSANSAG 430

DB 38 LCLSVPSVPSVTLSPQAQAAVGDLLHCEALRGSPPILYQFYHEDVTLGNSAASGG 97
QY 431 GVAISFSLTAHSGNYCTADNGFGPQSKAVSLISITVP 469
DB 98 GASFNLSLTAHSGNYSCAANGLGAQCEAVPVVISGP 136

RESULT 14
S00682
IGF Fc receptor alpha chain precursor - human
N:Alternate names: Fc-epsilon receptor
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S00682; B30154; S42209
A:Kochan, J.; Pattine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.
Nucleic Acids Res. 16; 3584; 1988
A:Title: Isolation of the gene coding for the alpha subunit of the human high affinity
A:Reference number: S00682; MUID:88233953; PMID:2967464
A:Molecule type: mRNA
A:Residues: 1-257 <KOC>
A:Cross-references: UNIPROT:P12319; EMBL:X06948; NID:G31317; PIDN:CAA30025.1; PID:G3131
R:Shinizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85; 1907-1911; 1988
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization
A:Reference number: A94191; MUID:88158102; PMID:2964640
A:Accession: B30154
A:Molecule type: mRNA
A:Residues: 1-257 <SHI>
A:Cross-references: GB:J03605; NID:G187449; PIDN:AAA36204.1; PID:G307164
R:Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.
Eur. J. Biochem. 220; 593-598; 1994
A:Title: High-level expression of the truncated alpha chain of human high-affinity recep
nant product.
A:Reference number: S42209; MUID:94170811; PMID:8125119
A:Accession: S42209
A:Molecule type: protein
A:Residues: 26-197 <YAG>
A:Experimental source: purified recombinant protein
C:Genetics:
A:Gene: GDB:FCER1A
A:Cross-references: GDB:119902; OMIM:147140
A:Map position: 1q23-1q23
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-257/Product: IGF Fc receptor alpha chain #status predicted <MAT>
F:44-95/Domain: immunoglobulin homology <IMM1>
F:125-178/Domain: immunoglobulin homology <IMM2>

Query Match 8.5%; Score 267; DB 2; Length 257;
Best Local Similarity 37.0%; Pred. No. 8.4e-11;
Matches 64; Conservative 26; Mismatches 73; Indels 10; Gaps 5;

QY 2 LLWVLLVLAQVSGQFATPPIIFLOPPTVFOGGRVTLTCGFFYFQPKTKWHRY 61
DB 10 LLCVALLFPAP-DGVLAQVQPKVSLAPPNRIIFGKGNVTLTCGNNFFVSVSTKWH-- 66
QY 62 LGKEILRETPDNI-----LEVQESGEYRCQAQGSPLSPVHLDFSSASLILQAPLS-VFEG 116
DB 67 -NGSLSEETSSNLINVAKFEDSGEYKCOHQVNESEPVYLEVFDWLLQLQASAEVVMG 125
QY 117 DSVILRCRAKAEVTLNNTI-YKNDNVLAFLNKRTHFPHACLKONGAYRCTG 168
DB 126 QPLFLRCHGRNWDVYKVIYKQGEALKYWNHNSITNATVEDSDSGTYCTG 178

RESULT 15
JL0118
Fc gamma (IgG) receptor Iia precursor - human
N:Alternate names: Fc gamma (IgG) receptor II (low affinity) alpha; surface glycoprotein
C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
 C/Accession: J01118; A31932; S02297; B45877; S00477; S02296
 R/Brooks, D.G.; Qiu, W.Q.; Luster, A.D.; Ravetch, J.V.
 J. Exp. Med. 170, 1369-1385, 1989
 A/Title: Structure and expression of human IgG FcRII (CD32): functional heterogeneity is
 A/Reference number: J01118; MUID:90010791; PMID:2529342
 A/Accession: J01118
 A/Molecule type: mRNA
 A/Residues: 1-317 <BRO>
 A/Cross-references: UNIPROT: P12318; GB: M31932; NID: g182473; PIDN: AAA35827.1; PID: g182474
 A/Experimental source: placenta
 A/Note: It is uncertain whether Met-1, Met-3, or Met-7 is the initiator
 R/Hibbs, M.B.; Bonadonna, L.; Scott, B.M.; McKenzie, I.F.C.; Hogarth, P.M.
 Proc. Natl. Acad. Sci. U.S.A. 85, 2240-2244, 1988
 A/Title: Molecular cloning of a human immunoglobulin G Fc receptor.
 A/Reference number: S02296; MUID: 88176920; PMID: 2965389
 A/Accession: A31932
 A/Molecule type: mRNA
 A/Residues: 3-317 <HIB>
 A/Cross-references: EMBL: J03619; NID: g183619; PIDN: AAA35932.1; PID: g306803
 R/Stuart, S.G.; Trounstein, M.L.; Vaux, D.J.T.; Koch, T.; Martens, C.L.; Mellman, I.; Mc
 J. Exp. Med. 166, 1668-1684, 1987
 A/Title: Isolation and expression of cDNA clones encoding a human receptor for IgG (Fc-
 A/Reference number: S02297; MUID: 88061079; PMID: 2824655
 A/Accession: S02297
 A/Molecule type: mRNA
 A/Residues: 1, 7, 3-317 <STU>
 A/Cross-references: EMBL: Y00644; NID: g31335; PIDN: CAA68672.1; PID: g31336
 A/Note: it is uncertain whether Met-1 or Met-7 is the initiator
 R/Seki, T.
 Immunogenetics 30, 5-12, 1989
 A/Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
 A/Reference number: A45877; MUID: 89307398; PMID: 2526077
 A/Accession: B45877
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 7-317 <SEK>
 A/Cross-references: GB: M28697; NID: g184841; PIDN: AAA36050.1; PID: g306928
 R/Stangelin, S.; Stamenkovic, I.; Seed, B.
 EMBO J. 7, 1053-1059, 1988
 A/Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity clon
 A/Reference number: S00477; MUID: 88296409; PMID: 3402431
 A/Contents: clone PC23
 A/Accession: S00477
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 7-317 <STE>
 C/Genetics:
 A/Gene: GDB: FCOR2A
 A/Cross-references: GDB: i119903; OMIM: 146790
 A/Map position: lq23-lq23
 C/Superfamily: FC gamma receptor III; immunoglobulin homology
 C/Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein
 F:1-35/Domain: signal sequence #status predicted <SIG>
 F:36-317/Product: IgG Fc receptor Iia #status predicted <REI>
 F:36-216/Domain: extracellular #status predicted <EXT>
 F:55-106/Domain: immunoglobulin homology <IMW1>
 F:136-189/Domain: immunoglobulin homology <IMW2>
 F:217-240/Domain: transmembrane #status predicted <TMW>
 F:241-317/Domain: intracellular #status predicted <INI>
 F:97,178/Binding site: carbohydrate (Asn) #status predicted

Query Match 8.5%; Score 264.5; DB 2; Length 317;
 Best Local Similarity 35.7%; Pred. No. 1.6e-10;
 Matches 70; Conservative 25; Mismatches 88; Indels 13; Gaps 6;

Qy 3 LWV-----ILLVLAPVSGQAPRPIFLPQPTWTFQGRVTLTKGRFYSPQKTKW 57
 Db 16 LWLQPLTVLLLSADSQAAPKAVLKLEPPWVNLQEDSVTLTCQAGSFESDIQW 75
 Qy 58 YHRYLGKILRETPDNI---LEVQESGEYRCQAGSPLSPVHLDFSSASLIQAP-LSV 113
 Db 76 FHN--GNLITHTQPSYRFKANNNDSEYTCQGTSLSDPVLTVLSEWLVLTQPHLEF 133

QY 114 PEGDSVWLRCRA-KAEVTLNNTIYKNDVLAFLNKRITDFHIPHACLKNDGAYRCTGYKES 172
 Db 134 QEGETIMLRCHSWKDKPLVKVTFQNGKSKFSLDPTFSIPQANHSHSGDYHCTG-NIG 192
 QY 173 CCFVSSNTVKIQVQEP 188
 Db 193 YTLFSSKEPVTITVQVP 208

Search completed: November 30, 2004, 11:51:09
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:28:00 ; Search time 198 Seconds
(without alignments)
1720.312 Million cell undamaged

Title: US-09-724-254A-3
 Perfect score: 3124
 Sequence: 1 MLLWILLVLAPVSGQPART.....AEFSLTHSFKNLFALSSFLP 592

Scoring table: BLOSUM62

DOCKING CASES:
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

```
Database :      UniProt_02:*
1:  uniprot_sprot:*
2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2949	94.4	977	2	Q96RD9	homo sapien
2	1193.5	38.2	734	2	Q96LA4	homo sapien
3	1193.5	38.2	734	2	Q96P31	homo sapien
4	1193.5	38.2	742	2	Q8N6S2	homo sapien
5	1186.5	38.0	740	2	Q8P6P29	homo sapien
6	927.5	29.7	582	2	Q8OWN2	mus musculus
7	847.5	27.1	619	2	Q96P30	homo sapien
8	826.5	26.5	515	2	Q96P35	homo sapien
9	820.5	26.3	515	2	Q96RE0	homo sapien
10	773.5	24.8	508	2	Q96LA5	homo sapien
11	773.5	24.8	508	2	AAQ88497	homo sapi
12	772	24.7	360	2	Q8N732	homo sapien
13	692.5	22.2	508	2	Q8BUA5	mus musculus
14	657.5	21.0	437	2	Q8NF56	homo sapien
15	600.5	19.2	509	2	Q96PQ5	m mman-g pr
16	599.5	19.2	509	2	Q91YK7	mus musculus
17	565	18.1	428	2	Q96PJ6	homo sapien
18	555	18.1	429	2	Q96LA6	homo sapien
19	548	17.5	124	2	Q6UY46	homo sapien
20	548	17.5	124	2	AAQ88452	homo sapi
21	548	17.5	366	2	Q8N759	homo sapien
22	543.5	17.4	154	2	Q8N733	homo sapien
23	537.5	17.2	422	2	Q96PJ3	homo sapien
24	452	14.5	722	2	Q6GNB3	Q6GNB3 xenopus lae
25	446.5	14.3	626	2	Q6DCH3	xenopus lae
26	428.5	13.3	357	2	Q8SPW5	macaca fasc
27	418.5	13.4	374	1	FC01_HUMAN	homo sapien
28	402.5	12.9	372	2	Q7YQJ5	caris famil
29	402.5	12.9	404	1	FC01_MOUSE	mus musculu
30	396	12.7	330	2	Q8R142	mus musculu
31	369	11.8	349	2	Q9MZT0	bos taurus

ALIGNMENTS

RESULT 1

Q96RD9	PRELIMINARY;	PRT;	977 AA.
ID	C96RD9;		
AC	Q96RD9;		
DT	01-DEC-2001 (TREMBlRel. 19, Created)		
DT	01-DEC-2001 (TREMBlRel. 19, Last sequence update)		
DT	01-WAR-2004 (TREMBlRel. 26, Last annotation update)		
DE	Fc receptor-like protein 5.		
Name=FCRH5;			
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_OX	[1]_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21396562; PubMed=11933702;		
RA	Davis R.S., Wang Y.H.; Kubagawa H.; Cooper M.D.;		
RT	"Identification of a family of Fc receptor homologs with preferential		
RT	B cell expression."		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).		
DR	EMBL; AF397453; AAK93971.1; -		
DR	HSP; P12319; IFZQ.		
DR	GO; GO:004872; F:receptor activity; IEA.		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003598; IG_c2.		
DR	Pfam; PF00047; Ig; 8.		
DR	SMART; SM00408; IGC2; 1.		
DR	PROSITE; PS50835; IG_LIKE; 8.		
KW	Receptor.		
SO	SEQUENCE		
SEQ	977 AA; 106496 MW; 2454A037B25509E7 CRC64:		

Query Match	94.4%;	Score 2949;	DB 2;	Length 977;
Best Local Similarity	98.3%;	Pred. No. 5e-204;		
Matches 562;	Conservative 2;	Mismatches 4;	Indels 4;	Gaps 1;
QY	1	MLLVWILLVLAPVSGQFARTPRIIIFLOQPWITVFOGERVITLTKGFRFYSPOKTKWHR	60	
Db	1	MLLVWILLVLAPVSGQFARTPRIIIFLOQPWITVFOGERVITLTKGFRFYSPOKTKWHR	60	
QY	61	YLKKEILRETPDNILEVQESGEYRCQAQSPSSPVHLDFSSASILIQAPLSVFFEGDSV	120	
Db	61	YLKKEILRETPDNILEVQESGEYRCQAQSPSSPVHLDFSSASILIQAPLSVFFEGDSV	120	
QY	121	LRCRAKAEVLTNNIIYKNDNVLAFLNKRITDFHPIHACLKDNGAYRCTGYKESCCPVSNT	180	
Db	121	LRCRAKAEVLTNNIIYKNDNVLAFLNKRITDFHPIHACLKDNGAYRCTGYKESCCPVSNT	180	
QY	181	VKIQVQEPFRNPVLRASSFQPIISGNPVTITCETQLSLERSDVLPRFRPRDDQTILGLWS	240	
Db	181	VKIQVQEPFRNPVLRASSFQPIISGNPVTITCETQLSLERSDVLPRFRPRDDQTILGLWS	240	
QY	241	LSPNFQITAMWKSQSGFYWCKAATMPHSVISDSPRSWIOVQIPASHPVLTISPEKALNPE	300	
Db	241	LSPNFQITAMWKSQSGFYWCKAATMPHSIIISDSPRSWIOVQIPASHPVLTISPEKALNPE	300	

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QY 301 GTKVTLHCETQEDSLRLTYRPFYHGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRLTYRPFYHGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVLSVTPVSHVPLNLSSPEDLI FEGAKVTLHCEAQRGLPLTYQFHEDAA 420
DB 361 LGAKPSKAVLSVTPVSHVPLNLSSPEDLI FEGAKVTLHCEAQRGLPLTYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVLSITVPVSHVPLTLSSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVLSITVPVSHVPLTLSSA 480
QY 481 EALTFCGATVTLCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLTEGHSNGNY 540
DB 481 EALTFCGATVTLCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLTEGHSNGNY 540
QY 541 CTADNGFGPQRSVSVLFTGCKWLASKPPL 572
DB 541 CTADNGFGPQRSVSVLFTV----VPVSRPIL 568

RESULT 2
Q96LA4 PRELIMINARY; PRT; 734 AA.
ID Q96LA4 AC Q96LA4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Fc receptor-like protein 3.
GN Name=FCRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396562; PubMed=114933702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
DR EMBL; AY043466; AAK91779.1; -.
DR HSSP; P12319; 1F2Q.
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 734 AA; 80827 MW; B359B494EBF12138 CRC64;

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Query Match 38.2%; Score 1193.5; DB 2; Length 734;
Best Local Similarity 45.5%; Pred. No. 1.9e-77;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 59
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 60
QY 60 RYLCKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
DB 61 ---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLDVHVEFSPDWLILQALHPVFEQDNV 116
QY 120 VLRCRAAEVTLNNTIYKNDNLVLAFLNKRDPFHIPACLDKNGAYRCTGVKESC---CPV 176
DB 117 ILRCQKDNKNTKQVYKDGKQLPNSYNLEKLTVNSVSRDNGSKYHCTAYRKFYILDIV 176
QY 177 SSNTVKIQVQEPFTRPVLRASSQPIISGNPVTLTCTQLSLERSDVPILRFRFRDQTLG 236
DB 177 SSNTVKIQVQEPFTRPVLRASSQPIISGNPVTLTCTQLSLERSDVPILRFRFRDQTLG 236

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DB 177 TSKPLNIQVQLFLHPVLRASSPTIEGSPMTLTCTQLSPQRPDVQLQSLFRDSQTLG 236
QY 237 LGWSLSPNFQITAMWSKDSGYWCKAATMHSVITSDSPRSWIOVQ-IPASHVTLTSPK 295
DB 237 LGWSRSPRLQIPAMWTEDSGYWCEVETVTHSIKKRSQRVQVFEVSNVLEIRPTG 296
QY 296 ALNPEGTKVTLHCETQEDSLRLTYRPFYHGVPLRHKSVRCERGASISFSLT---ENSGN 352
DB 297 GOLLEGENNVILCVAGQSGTTFVSHKKG-RVRSRGRKQVRSLLAEHLVTLVKESDAGR 355
QY 353 YYCTADNGLGAKPSKAVLSVTPVSHVPLNLSSPEDLI FEGAKVTLHCEAQRGLPLTY 412
DB 356 YYCAADNVHSPILSTWIRVTVRIPVSHVPLTFRAPRAHTVVGDLLELHCESLRGSPPILY 415
QY 413 QPHHDAALERRSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVLSITVPVSH 472
DB 416 RYFHEDVTLGNSSAPSGGASFNLSLTAHSGNYSCTADNGLGAQHGVSRLVTVPSVR 475
QY 473 PVLTLSSAEALTFCGATVTLHCEVORGSPQILYQFYHEDMPLVSSTPSVGRVSFSLT 532
DB 476 PVLTLRAFGAQAQVVGDLLELHCESLRGSFPILYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EGHSGNYYCTADNGFGPQRSVSVLFTVG 561
DB 536 TEHSGNYSCEADNGLGAQHSKVTNLNVTG 564

RESULT 3
Q96P31 PRELIMINARY; PRT; 734 AA.
ID Q96P31 AC Q96P31;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Xu M.-J., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416901; AAL3290.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
SQ SEQUENCE 734 AA; 80855 MW; B3411B7A3A5EC668 CRC64;

Query Match 38.2%; Score 1193.5; DB 2; Length 734;
Best Local Similarity 45.5%; Pred. No. 1.9e-77;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 59
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPMTTVFQGERVTLTKGFRFVSPQ-KTKWYH 60
QY 60 RYLCKEILRETPDNILEVQESGEYRCQAQSPVHLDFFSSASLILQAPLSVFEQDSV 119
DB 61 ---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLDVHVEFSPDWLILQALHPVFEQDNV 116
QY 120 VLRCRAAEVTLNNTIYKNDNLVLAFLNKRDPFHIPACLDKNGAYRCTGVKESC---CPV 176
DB 117 ILRCQKDNKNTKQVYKDGKQLPNSYNLEKLTVNSVSRDNGSKYHCTAYRKFYILDIV 176
QY 177 SSNTVKIQVQEPFTRPVLRASSQPIISGNPVTLTCTQLSLERSDVPILRFRFRDQTLG 236
DB 177 TSKPLNIQVQLFLHPVLRASSPTIEGSPMTLTCTQLSPQRPDVQLQSLFRDSQTLG 236

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QY 237 LGWSLSNFOITAMWSKDSGYFWCKAATPHSVISDPSRWIQV-IPASHPVLTLSPEK 295
D 237 LGWSRSRLQIPAMWTDSSGYCEVETVTHSIKSLRSQIRVQRPVSVNNVLEIRPTG 296
QY 296 ALNPEGTQVTLHCETQDSRLTYRHYHGVPLRHKSVCRCASISFSLTT---ENSGN 352
D 297 GQLIEGNMVLICSAVAGSGTTFVSWHKEG-RVRSIGRKTQRLSLAELHVLTVKESDAGR 355
QY 353 YYCTADNGLGAKPSKAVSLGVTPVSHPVNLNLSPEDLIEGAKVTLHCEAQRGSLPIY 412
D 356 YYCAADNVHSPILSTWIRVTPVSHPVLTFRAPRAHTVVGDLLEHCSLRGSPPIY 415
QY 413 QFHEDAALERRANSAGGVAISFSLTAHSGNYCTADNGPQPSKAVSLITVPVSH 472
D 416 RPYHEDVTGNSAPSGGASFNLSLTAHSGNYSCDADNGLGAQSHGVSLVTPVSR 475
QY 473 PVLTLSSAALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSFSLT 532
D 476 PVLTRAPGAQAVVGDLLEHCSLRGSPPIYVFWHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EHGSGNYCTADNGFGPQRSEVSLFVTG 561
D 536 TEHSGNYSCEADNGLGAQSHKVTLNVTG 564

RESULT 4
Q8N6S2 PRELIMINARY; PRT; 742 AA.
AC Q8N6S2
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE FCRH3 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC028933; AAH28933.1; -.
DR HSSP; P12319; 1F20.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SMO0408; IGC2; 1.
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DR SMART; SMO0408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 6.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
SQ SEQUENCE 742 AA; 81853 MW; B06502007CAl9B8 CRC64;

Query Match 38.2%; Score 1193.5; DB 2; Length 742;
Best Local Similarity 45.5%; Pred. No. 1.9e-77;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPO-KTKAYH 59
D 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFOGERVTLTKGFRFYSPO-KTKAYH 59
QY 60 RYLGEIILRETPDNILEVQESGEVRCOAGSPPLSPVHLDSESSALILQAPLSVFECDV 119
D 61 ---DKELIKIKHDKI-QITEPGNYCKTRGSSLSDAVHVEFSPDWLILQALHPVFECDV 116
QY 120 VLRCRAKAEVTLNNTIYKNDVLAFLNKRTHPHACLKONGAYRCYGYKESC---CPV 176
D 117 ILRCQKQKNTKHQVYVYKQKQLENVYNLEKITVNSYSRDNKSYHCYAYRKFYILDIEV 176
QY 177 SNTVKIQVOEPTFRPLVRASSFQIPSGNPVLTCTCTSLERSDVLPRFRFRDQTLG 236
D 177 TSRLNIQVOELFLHPVLRASSSTFIEGSPMLTCTCTQSPQPDVQLQSLFRDSQTLG 236
QY 237 LGWSLSPNFQITAMWSKDSGYFWCKAATPHSVISDPSRWIQV-IPASHPVLTLSPEK 295
D 237 LGWSRSRLQIPAMWTDSSGYCEVETVTHSIKSLRSQIRVQRPVSVNNVLEIRPTG 296
QY 296 ALNPEGTQVTLHCETQDSRLTYRHYHGVPLRHKSVCRCASISFSLTT---ENSGN 352
D 297 GQLIEGNMVLICSAVAGSGTTFVSWHKEG-RVRSIGRKTQRLSLAELHVLTVKESDAGR 355
QY 353 YYCTADNGLGAKPSKAVSLGVTPVSHPVNLNLSPEDLIEGAKVTLHCEAQRGSLPIY 412
D 356 YYCAADNVHSPILSTWIRVTPVSHPVLTFRAPRAHTVVGDLLEHCSLRGSPPIY 415
QY 413 QFHEDAALERRANSAGGVAISFSLTAHSGNYCTADNGPQPSKAVSLITVPVSH 472
D 416 RPYHEDVTGNSAPSGGASFNLSLTAHSGNYSCDADNGLGAQSHGVSLVTPVSR 475
QY 473 PVLTLSSAALTFEGATVTLHCEVQRGSPQILYQFYHEDMPLVSSSTPVSGRVSFSLT 532
D 476 PVLTRAPGAQAVVGDLLEHCSLRGSPPIYVFWHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EHGSGNYCTADNGFGPQRSEVSLFVTG 561
D 536 TEHSGNYSCEADNGLGAQSHKVTLNVTG 564

RESULT 5
Q96P29 PRELIMINARY; PRT; 740 AA.
AC Q96P29
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE SH2 domain-containing phosphatase anchor protein 2c.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M.-J., Zhao Z.J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF416903; AAL13292.1; -.
DR HSSP; P12319; 1F20.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00047; Ig; 4.
DR SMART; SMO0408; IGC2; 1.
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1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRYSPO-KTKWYH 59
1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRYSPO-KTKWYH 60
60 RYLKGTRETPDNILEVQESGEYRCQAQSPSSPVHLDFFSSASLILOAPLSVFEQDSV 119
61 ---DEKLLKIKHDKI-QITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEQDNV 116
120 VLRCRAKAEVTLNNTIYK-NDNVLAFLNKRDTFPHIACLDKNGAYRCTGYKESCCPVSSN 176
117 ILRCQGDNDKNTKOKVYKDGKOLPNSYNLEKITVNSVSDNSKYHCTAYRKYVILDIIEV 176
177 SSNTVKIQOEFPRPY-----LRASSFQIPISGNPVTLTCEQLSLERSDVLPRFRFR 230
177 TSKEPNILOVQV---PVSNNLEIRPTGGQLIEGENWVLC-----SVAQSGGIVTWSHK 229
231 DDQTLGLG----WLSLSPNFQITAMWSKDSGFYCKAATMPSHVSISDPSRWIQ--VOIPA 284
230 EGRVSLGRKTRQSLAELHVLTVKESDAGRYCAADNVHSPILS-----TWIRVTVRIPV 285
285 SHPVLTLSPEKALNFEGTKVTLHCETOEDSLRTLYRYHGVLPRLHKSVCERCASISFS 344
286 SHPVLTFRAPRAHTVWGDLELHCELSRGSPPIILYRYHEDVTLGNSAFSGGAGFNLS 345
345 LTTENSGNYCTADNGLGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEAGKVTLHCEAQ 404
346 LTAHSGNYSADNGLGASHGVSLRVTPVSRPVLTLRAPGAQVWGDLELHCESL 405
405 RGSPLILYQFHEDAAELRRSAGGVAISFSLTAHSGNYYCTADNGLGKPSKAVSL 464
406 RGSFPILYFYHEDDTLGNISAHSGGASFNLSLTTBHSNYSCEADNGLGAKHRSKVVTL 465
465 SIT-----VPVSHPVTLTSSAEALTFFEGATVTLHCEVQVQSP 501
466 NVGTSTSRNRTLTAAGITGLVLSI-----LVLAALHLLHVARARXP 508

RESULT 8
Q96PJ5 PRELIMINARY; PRT; 515 AA.
AC Q96PJ5 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE IFGP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Tonsil;
RX MEDLINE=20033006; PubMed=12037601;
RA Guselnikov S.V., Ershova S.A., Mechetina L.V., Najakshin A.M.,
RA Volkova O.Y., Alabyev B.Y., Taranin A.V.,
RT "A family of highly diverse human and mouse genes structurally links
RT leukocyte FcR, gp42 and PECAM-1";
RL Immunogenetics 54:87-95(2002).
DR EMBL; AF329490; AAL23900.1; -.
DR HSSP; P12319; IF2Q.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
SQ SEQUENCE 515 AA; 57224 MW; F3B7AD14FB1B449A CRC64;
Query Match 26.5%; Score 826.5; DB 2; Length 515;
Best Local Similarity 43.5%; Pred. No. 3.7e-51;
Matches 184; Conservative 55; Mismatches 161; Indels 23; Gaps 6;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRYSPOKTKWYH 60

1 MLLWASILLAPVCGQSAAHKPVISVHPWTTTFFKGERVTLTNCNGFQFVATEKTTWYHR 60
61 YLGEKILRETPDNILEVQESGEYRCQAQSPSSPVHLDFFSSASLILOAPLSVFEQDSV 120
61 HWGKGLTLPONTLEVRSSGLYRCQARSPSPVRLFFSSDSLILOAPYSVFEQDTLV 120
121 LRCRAKAEVTLNNTIYK-NDNVLAFLNKRDTFPHIACLDKNGAYRCTGYKESCCPVSSN 179
121 LRCHRRREKLTAVKYTWNGNLSKNSKDWLLIPOASSNNNGNYRCIGYGDENDVFRSN 180
180 TVKIQOEFPRPYLRASSFQIPISGNPVTLTCEQLSLERSDVLPRFRFRDDQTLGLGW 239
181 FKIIKIQELFHPPELKATDSQTEGNSVNLSCETQLPERSDTPLHFNFRDGEVILSDW 240
240 SLSPNFQITAMWSKDSGFYCKAATMPSHVSISDPSRWIQV-IPASHVTLTLPSEKALN 298
241 STYPELOLPTVWRENSGSGWCAETVRGNIHKHSPSLQIHVQIPVSGVLTLETPSGGQA 300
299 FEGTKVTLHCETOEDSLRTLYRYHGV-PLRHKSVCERCASISFSLTTEHSGNYCT 356
301 VEGLMLVLVCSVAEGTGTTFSSHREDQESLGRKTQSLRAELPELPAIROSHAGGYCT 360
357 ADNGLGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEAG-----KVTLHCEAQ 404
361 ADNSYG--PVQSNVNLVTRTP-----GNRDLVAAGATGGLLSALLLAVALLPFCWRR 413
405 RGS 407
414 RKS 416

RESULT 9
Q96RE0 PRELIMINARY; PRT; 515 AA.
AC Q96RE0 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Fc receptor-like protein 4.
GN Name=FCRH4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=21395652; PubMed=11493702;
RA Davis R.S., Wang Y.H., Kubagawa H., Cooper M.D.;
RT "Identification of a family of Fc receptor homologs with preferential
RT B cell expression";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9772-9777(2001).
DR EMBL; AF397452; AAK93970.1; -.
DR HSSP; P12319; IF2Q.
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Receptor.
SQ SEQUENCE 515 AA; 57250 MW; 32FBD6FAB2B19D3D CRC64;
Query Match 26.3%; Score 820.5; DB 2; Length 515;
Best Local Similarity 43.3%; Pred. No. 1e-50;
Matches 183; Conservative 55; Mismatches 162; Indels 23; Gaps 6;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRYSPOKTKWYH 60
1 MLLWASILLAPVCGQSAAHKPVISVHPWTTTFFKGERVTLTNCNGFQFVATEKTTWYHR 60
61 YLGEKILRETPDNILEVQESGEYRCQAQSPSSPVHLDFFSSASLILOAPLSVFEQDSV 120


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QY 163 AYRC-TGYKSCCPVSNVTKIOVQBPFRPVLRASSFOIPISGNFVTLTCTQLSLERSD 221
Db 79 NYFCSTKGGFLWDKTSNVKIKVQLFQRPVLTASSFOIPEGGFSVSLKCTETLSFQRLD 138
QY 222 VPLRFFPRDDQTLGLGWSLSPNFQITAWKSDSGFYWCKAATMPSHVSIDSFSRWIQVQ 281
Db 139 VQLOQCFRQNLVSGWSSSPLOLSAVWSEDTGYSWCKAETVTHRIKQLSQSIHQV 198
QY 282 -IPASHPVLTLSPEKALNPEGTAVTLHCETQEDSLTLYRFYHE--GVPLRHKSVCRCRG 338
Db 199 RIPSINVSLEIRAPGQVTEGQKLLILCSVAGTGNVTSWYEEATGTSMGKKTQR--- 254
QY 339 ASISFSL-----TTSNGNYCYCTADNGLGAKPSKAVSLSVTPVSHPVNLNLSPEDLIFE 393
Db 255 -SLSAELEIPAVKESDAGKYCYCRADNGHVPISQKVVNIPVIRFVSFVLTLSRSPGQAARV 313
QY 394 GAKVTLHCEAQRSLPLTYOFHEDAALEERSANSAGGVAISFLTAHSGNYCYCTADNG 453
Db 314 GDLELHCEALRSPPLTYOFYHEDVTLGNSSAPSGGASFNLSLTAHSGNYSCANNNG 373
QY 454 FGORSKAVSLISITVP 469
Db 374 LGAQCSAVPVSISGP 389

RESULT 12
Q8N732 PRELIMINARY; PRT; 360 AA.
ID Q8N732
AC Q8N732;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE DJ801G22.1 (Novel immunoglobulin domain protein similar to
immunoglobulin receptors) (Fragment).
GN Name=dJ801G22.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL135929; CAB92793.1; -.
DR HSSP; F12319; IFQ.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IGLIKE; 4.
KW Receptor.
FT NON_TER 1
FT NON_TER 360
SQ SEQUENCE 360 AA; 40724 MW; 7ACC2B7FA3256D62 CRC64;

Query Match 24.7%; Score 772; DB 2; Length 360;
Best Local Similarity 46.1%; Pred No. 2e-47;
Matches 165; Conservative 49; Mismatches 138; Indels 6; Gaps 4;

QY 22 RPIILQPPWTVTFQGERVLTCKGFRFYPSPQTKWYHYLGKEILRTPNILEVQBSG 81
Db 4 KPVISVHPPTWTFKXGERVLTLCNGFQFYATEKTTWYHRYWGEKLTLPNTLEVRSG 63
QY 82 EYRCQAGSPLSPVHLDPSSASLILOAPLSVFEGDSVVLRCRAEYTLNNTYK-NDN 140
Db 64 LYRCQAGSPRNPRVLLFSSLSLILOAPYSVFEGDVLVLRCHRRKREKLTAVKWTWGN 123
QY 141 VLAFLNKRDFEIPHACLKDNCAVRCYTKYKSCCPVSNVTKIOVQBPFRPVLRASSFO 200
Db 124 ILSISNKSNDLLIPQASSNNNGYRCIGYGDENDVFRSFKIKIQLFPHPELKATDSQ 183

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QY 201 PISGNPVLTCTQLSLERSDVLPRFRDDOTLGLGWSLSPNFQITAWKSDSGFYWC 260
Db 184 PTEGNSVNLSCETQLPERSDTPLHFNFRDGEVILSDWSTYPELQLPTVWRENSGSYWC 243
QY 261 KAAATMPSHVSIDSFSRWIQVQ-IPASHPVLTLSPEKALNPEGTAVTLHCETQEDSLTLY 319
Db 244 GAETVRGNIHKHSPSLQIHVQRIPVSGVLLLETOPSGGQAVEGEMLVLCVSAEQTGDTTF 303
QY 320 RFYHEGV--PLRHKSVCRCGASFSFLTTSNGNYCYCTADNGLGAKPSKAVSLSVTV 375
Db 304 SWHREDQESLGRKTRQSLRAELPAIROSHAGGYCTADNSYG--PVQSWVLNVTV 359

RESULT 13
Q8BJAS PRELIMINARY; PRT; 508 AA.
ID Q8BJAS
AC Q8BJAS;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Mus musculus activated spleen cDNA, RIKEN full-length enriched
library, clone:F830015F10 product:weakly similar to SH2 DOMAIN-
CONTAINING PHOSPHATASE ANCHOR PROTEIN 1C.
DE Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA Kanno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K.; Itoh M.; Aizawa K.; Nagaoka S.; Sasaki N.; Carninci P.;
RA Kanno H.; Akiyama J.; Nishi K.; Kusunai T.; Tashiro H.; Itoh M.;
RA Yumoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;
RA Fujiwaki S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watanabe M.;
RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai J.;
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]

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RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089756; BAC40954.1; -.
DR HSSP; P12319; 1F2Q.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG LIKE; 4.
SQ SEQUENCE 508 AA; 56795 MW; 27774A4733A9443F CRC64;

Query Match 22.2%; Score 692.5; DB 2; Length 508;
Best Local Similarity 40.9%; Pred. No. 1.7e-41;
Matches 160; Conservative 63; Mismatches 131; Indels 37; Gaps 6;

QY 105 LILQAPLSVEGDSVLRCAKAEVTLNN-TIYNNDNVLAFLNKRDTDFPHACLKDNGA 163
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 LVLQAPPAVFEGDSVLRCAKAGIEAETLTFYKDGKALFLHPQSSELYIHANLKDNGQ 90
QY 164 YRCTGYKESC--CPVSNNTKIQVQEPFTRPVLRASFPQISGNPVLTCETQLSLERSD 221
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 91 YKTSKKKWSFGSLYTSNTRVQVELFRPVLRLARPSHPIDGSPVTLTCQTLSAQKSD 150
QY 222 VPLRFPRFRDDQTLGLGWSLSPFOITAMWSDSGFYCKAAATWPHSVISDSRSPRIQVQ 281
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 151 ARLQFCFRNLQLLGGSCRSSEPHIPAIVTESKRYQCKAEIVNSQVRKQSTAFILPQV 210
QY 282 IPASHPVLTLSPEKALNFEGTKVTLHCETOEDSLRTLRYRPHGVF-----LRH 330
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 211 RASARFQTHIIPASKLVFEGQLLLNCV-----KGVPGLKFSWKYKMDLN 257
QY 331 KSVRCERGASISPLTTEN---SGNYCTADNGLGAKPKSKAVLSVTVPVSHVPLNLSRP 387
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 258 KEYILKSSNAEFKISQVNSDAGEVHREATNRRSFVSAPFIIITKVPVSPQVLTLSG 317
QY 388 EDLIFEKAKVTLHCEAQRGSLPILYQFHEDAAALERRSANSAGVAISFSLTAHSGNYY 447
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 318 KQALEGLMTLHCQSQRGSPCLYEFYFENVSLGNSSILSGGAYFNFSMSTERSGNYY 377
QY 448 CTADNGFGPQSKAVLSLSI-----TVPVS 471
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 378 CTADNGLGACQCSAIRISIFDMTKNSRVPWA 408

RESULT 14
Q8NF56 ID Q8NF56 PRELIMINARY; PRT; 437 AA.
AC Q8NF56;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE FIJ00333 protein (Fragment).
GN Name=FIJ00333;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS0835; IG LIKE; 3.
FT NON_TER 1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

Query Match 21.0%; Score 557.5; DB 2; Length 437;
Best Local Similarity 50.5%; Pred. No. 4.7e-39;
Matches 140; Conservative 29; Mismatches 101; Indels 7; Gaps 2;

QY 291 LSPKALNFEGTK-----VTLHCETOEDSLRTLRYRPHGVFVHGVPLRHKSVCRCGASISFS 344
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 24 LAPSPSGFPGAQAVVGDLLHCEAPRGSPPILYWFYHEDVTLGSSAPSGGASFNLS 83
QY 345 LTTNSGNYYCTADNGLGAKPKSKAVLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQ 404
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 84 LTAHSGNYSCEANGLVAQHSDTISLSVIVFVSRPILTFRAPRAQAVVGDLLHCEAL 143
QY 405 RGSPLILYQFHEDAAALERRSANSAGVAISFSLTAHSGNYYCTADNGFGPQSKAVSL 464
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 144 RGSPLILYWFYHEDVTLGKISAPSGGASFNLSLTTHSGIYSCDANGLEAQSEWVTL 203
QY 465 SITVPVSHVPLTLSSAALTFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGR 524
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 204 KVAVPVSRLTLRAPGTHAAVGDLLHCEALRGSPPILYRPFPHEDVTLGNRSPS-GG 262
QY 525 VSFPSLITGHSNGNYYCTADNGFGPQSKAVLSVLEVTG 561
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 263 ASLNLSTLAHSGNYSCEADNGLGAQRSETVTLITG 299

RESULT 15
Q9EQY5 ID Q9EQY5 PRELIMINARY; PRT; 509 AA.
AC Q9EQY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MMAN-g protein precursor (IFGP2) (Mus musculus adult male diencephalon
DE cDNA, RIKEN full-length enriched library, clone:9310158F12
DE product:macrophage scavenger receptor 2, full insert sequence) (Mus
DE musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2810439C17 product:macrophage scavenger
DE receptor 2, full insert sequence).
GN Name=MsR2; Synonyms=MMAN-g;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoshimoto M., Matsumoto K., Ukai Y., Kitamura K.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090423; BAC03404.1; -.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS0835; IG LIKE; 3.
FT NON_TER 1
SQ SEQUENCE 437 AA; 46521 MW; F56DED36523E52CA CRC64;

Query Match 21.0%; Score 557.5; DB 2; Length 437;
Best Local Similarity 50.5%; Pred. No. 4.7e-39;
Matches 140; Conservative 29; Mismatches 101; Indels 7; Gaps 2;

QY 291 LSPKALNFEGTK-----VTLHCETOEDSLRTLRYRPHGVFVHGVPLRHKSVCRCGASISFS 344
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 24 LAPSPSGFPGAQAVVGDLLHCEAPRGSPPILYWFYHEDVTLGSSAPSGGASFNLS 83
QY 345 LTTNSGNYYCTADNGLGAKPKSKAVLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQ 404
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 84 LTAHSGNYSCEANGLVAQHSDTISLSVIVFVSRPILTFRAPRAQAVVGDLLHCEAL 143
QY 405 RGSPLILYQFHEDAAALERRSANSAGVAISFSLTAHSGNYYCTADNGFGPQSKAVSL 464
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 144 RGSPLILYWFYHEDVTLGKISAPSGGASFNLSLTTHSGIYSCDANGLEAQSEWVTL 203
QY 465 SITVPVSHVPLTLSSAALTFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGR 524
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 204 KVAVPVSRLTLRAPGTHAAVGDLLHCEALRGSPPILYRPFPHEDVTLGNRSPS-GG 262
QY 525 VSFPSLITGHSNGNYYCTADNGFGPQSKAVLSVLEVTG 561
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 263 ASLNLSTLAHSGNYSCEADNGLGAQRSETVTLITG 299
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RN [4] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=21085660; PubMed=11217811;
 RA RIKEN FANTOM Consortium;
 RL "Functional annotation of a full-length mouse cDNA collection."
 RN [5] Nature 409:685-690(2001).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=20499374; PubMed=11042159;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RL "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RN [6] Nature 420:563-573(2002).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RN Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RL "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes."
 RN [7] Genome Res. 10:1617-1630(2000).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon, and Whole body;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RN Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishigaki T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RL "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer."
 RN [8] Genome Res. 10:1757-1771(2000).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RN Hayashida K., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Fukushida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RN Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RN Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RN Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akimura T., Akimura T., Aono H., Arai A.,
 RN Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RN Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RN Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RN Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RN Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
 RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB028174; BAB18569.1; -
 DR EMBL; AF329486; AAL23896.1; -
 DR EMBL; AK034125; BAC28595.1; -
 DR EMBL; AK076123; BAC36201.1; -
 DR MGD; MGI:1933397; Msr2.

DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR001190; Strc_receptor.
 DR Pfam; PF00047; ig_3.
 DR Pfam; PF00530; SRCR_1.
 DR PRINTS; PRO0258; SPERACTRCPTR.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00202; SR; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00420; SRCR_1; 1.
 DR PROSITE; PS0287; SRCR_2; 1.
 KW Receptor; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 509 Potential.
 SQ SEQUENCE 509 AA; 55787 MW; EAB422EAC1310ECC CRC64;
 Query Match 19.2%; Score 600.5; DB 2; Length 509;
 Best Local Similarity 30.4%; Pred. No. 7,6e-35;
 Matches 147; Conservative 71; Mismatches 159; Indels 107; Gaps 8;
 QY 96 VHLDFSSASLILQAPLSVPEGSVVLRCRAKAEVTLNNTIYKDNV-LAPLNKRTDFHIP 154
 Db 15 VQSDWLSISL-----PHRSYEGDQVVISCTGKNGDKLKYFKDGYHETVSSASYTIR 70
 QY 155 HACLKONGAYRCTGYKESCCPV-----SNTVKIQVEPTFRVLRASSFQPSIGNPVILT 210
 Db 71 NARRGDSGYSCKADRKFLFDITTEGSKWLNQVLEFPAPCLTASLPQVEGSSVTL 130
 QY 211 CETQLSLERSDVLPFRFRDDQTTLGLWLSLPNFQITAMWSKDSGFYWCKAATPHSVI 270
 Db 131 CNTWLPSTRATQLRVSPFKDGTILQSGWT-SSKFTISAISKEDSGNYWCCEAMTASRVS 189
 QY 271 SPSPRSNIOVQ-IPASHPVLTLSPEKALNFEKTVLHCETQEDSLRTLYRYHGVPLR 329
 Db 190 KQSHRSYIDVERIPVSQVTMEIQPSRGWGVG----- 221
 QY 330 HXSVRCERGASISFSLTTENSGNYICTADNGLGAKPSKAVLSVTPVPSHPVLNLSPPD 389
 Db 222 -----EP 223
 QY 390 LIPEGAKVTLHCEAQRGSLPIYQPHEDA--ALERRSANSAGGVAISFSLTAHSGNY 447
 Db 224 LVVEGEPVLVACSVAKGTGLITFSWHRQDTKESVGKKSQRQORVELEIPTIRESHAGGY 283
 QY 448 CTADNCGFQPSKAVLSLITVPVSHPVLTLSAEALTPEGATVTLHCEVQRGSPQILYQF 507
 Db 284 CTADNNYGLIQSAIVNITVKIPVNLPLLSISVPGVLPFGDVAELHCEDKRASPPVLYWF 343
 QY 508 YHEDMPLVSSSTPSVGRVSFSLTEGHSGNYICTADNCGFQPSRSEVSLFTVTKCWLA 567
 Db 344 YHENITLANTSAPFGGKASFKLSTAGHSGNYSCEAENAWGKRSEVVTLNVT----- 396
 QY 568 SKPP 571
 Db 397 -EPP 399

Search completed: November 30, 2004, 11:50:23
 Job time : 202 secs

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Adm35234 Human LY1
Adp18669 Human pro
Abp75420 Human sec
Abu99156 Novel hum
Abu99157 Novel hum
Adm93877 Human NOV
Abu99158 Novel hum
Adm93881 Human NOV
Adm35268 Human LY1
Adm35239 Human imm
Aab82317 Human LY1
Adm35264 Human LY1
Adf89715 Human can
Adl06539 Human tum
Adf74334 Extracell
Adf74316 Human FCR
Adp63021 Human pol
Adm35277 Human LY1
Adm35273 Human LY1

26 826.5 26.5 515 7 ADM35234
27 826.5 26.5 515 8 ADP18669
28 826 26.4 167 6 ABP75420
29 803.5 25.7 421 6 ABU99156
30 803.5 25.7 421 6 ABU99157
31 803.5 25.7 421 8 ADM93877
32 786.5 25.2 421 6 ABU99158
33 786.5 25.2 421 8 ADM93881
34 783.5 25.1 445 7 ADM35268
35 773.5 24.8 508 4 AAB82317
36 773.5 24.8 508 7 ADM35239
37 773.5 24.8 508 7 ADM35264
38 773.5 24.8 508 8 ADP83715
39 773.5 24.8 508 8 ADL06539
40 769.5 24.6 380 7 ADF74334
41 769.5 24.6 489 7 ADF74316
42 745 23.8 406 8 ADM93879
43 729.5 23.4 327 5 ABP63021
44 713 22.8 397 7 ADM35277
45 703 22.5 460 7 ADM35273

ALIGNMENTS

RESULT 1
AAB82314
ID AAB82314 standard; protein; 592 AA.
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AC AAB82314;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human immunoglobulin receptor isoform IRTA2b.
XX
KW Immunoglobulin superfamily receptor translocation associated; IRTA;
KW IRTA2b; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
KW myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT Protein 16..592
FT Modified-site 132..134
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 383..385
FT Modified-site /note= "Asn is N-glycosylated"
XX
WO200138490-A2.
XX
31-MAY-2001.
XX
28-NOV-2000; 2000WO-US032403.
XX
29-NOV-1999; 99US-0168151P.
XX
(UYCO) UNIV COLUMBIA NEW YORK.
XX
Dalla-Favera R;
XX
WPI; 2001-385921/37.
XX
N-PSDB; AAF30951.
XX
New genes encoding immunoglobulin receptor. Immunoglobulin super Receptor
Translocation Associated proteins, used to treat B cell malignancies
including lymphomas and multiple myeloma.
XX
Claim 3; Fig 18B-1-18B-2; 72pp; English.
XX
The present sequence is that of the novel human immunoglobulin receptor,
CC

26 826.5 26.5 515 7 ADM35234
27 826.5 26.5 515 8 ADP18669
28 826 26.4 167 6 ABP75420
29 803.5 25.7 421 6 ABU99156
30 803.5 25.7 421 6 ABU99157
31 803.5 25.7 421 8 ADM93877
32 786.5 25.2 421 6 ABU99158
33 786.5 25.2 421 8 ADM93881
34 783.5 25.1 445 7 ADM35268
35 773.5 24.8 508 4 AAB82317
36 773.5 24.8 508 7 ADM35239
37 773.5 24.8 508 7 ADM35264
38 773.5 24.8 508 8 ADP83715
39 773.5 24.8 508 8 ADL06539
40 769.5 24.6 380 7 ADF74334
41 769.5 24.6 489 7 ADF74316
42 745 23.8 406 8 ADM93879
43 729.5 23.4 327 5 ABP63021
44 713 22.8 397 7 ADM35277
45 703 22.5 460 7 ADM35273

2002273

Total number of hits satisfying chosen parameters: 2002273

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : A_Geneseq_23Sep04: *
1: Geneseq1980s: *
2: Geneseq1990s: *
3: Geneseq2000s: *
4: Geneseq2001s: *
5: Geneseq2002s: *
6: Geneseq2003as: *
7: Geneseq2003bs: *
8: Geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match %	Length	ID		
1	3111	99.6	592	AAB82314	Aab82314	Human imm
2	3111	99.6	592	ADM35236	Adm35236	Human LY1
3	2950	94.4	759	AAB82313	Aab82313	Human imm
4	2950	94.4	759	ADM35235	Adm35235	Human LY1
5	2950	94.4	977	AAB82315	Aab82315	Human imm
6	2950	94.4	977	ABP97215	Abp97215	Tumour-as
7	2950	94.4	977	ADM35237	Adm35237	Human LY1
8	1193.5	38.2	582	ABU99155	Abu99155	Novel hum
9	1193.5	38.2	582	ADM93875	Adm93875	Human NOV
10	1193.5	38.2	707	ADM06089	Adm06089	Human pro
11	1193.5	38.2	734	AAB82316	Aab82316	Human imm
12	1193.5	38.2	734	ADM35238	Adm35238	Human LY1
13	1193.5	38.2	733	ADL06557	Adl06557	Human tum
14	1176	37.6	727	AB384668	Abb84668	Human SEC
15	1150.5	36.8	554	ADP74336	Adp74336	Extracell
16	1150.5	36.8	717	ADF74337	Adf74337	Human FCR
17	1150.5	36.8	717	ADF74318	Adf74318	Human FCR
18	1120	35.9	222	ABP69283	Abp69283	Human pol
19	900	28.8	181	ABP51264	Abp51264	Human MDD
20	900	28.8	181	ABP51409	Abp51409	Human MDD
21	889.5	28.5	570	ADP74389	Adp74389	Murine Fc
22	889	28.5	468	ADP74391	Adp74391	Extracell
23	847.5	27.1	639	ADJ70604	Adj70604	Human rea
24	826.5	26.5	515	AAB82312	Aab82312	Human imm
25	826.5	26.5	515	AB80608	Abb80608	Human 85g

CC immunoglobulin superfamily receptor translocation associated protein
CC isoform 2b (IRTA2b), an FC receptor involved in the pathogenesis of
CC lymphoma and melanoma. Efforts to identify genes involved in chromosomal
CC aberrations affecting band Ig21 in multiple myeloma and B cell lymphoma
CC led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding
CC members of a novel subfamily of related receptors within the
CC immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA
CC isoforms, IRTA2a and IRTA2c (see also AAB82314 and AAB82315).
CC IRTA2b is a 592 amino acid glycoprotein, which diverges from IRTA2a at
CC residue 560, extending for a further 32 residues, whose hydrophobicity
CC suggest docking to the plasma membrane via a GPI anchor. The IRTA2 genes
CC display a specific pattern of expression in mature B cells. IRTA2 is
CC expressed in GC centrocytes and in perfollicular cells, which may
CC include immunoblasts and memory cells. The invention provides IRTA
CC nucleic acids and proteins, and antibodies directed to an epitope of an
CC IRTA protein. Methods are claimed for: detecting a B cell malignancy
CC comprising a Ig21 chromosomal rearrangement using a nucleic acid molecule
CC that specifically hybridises with a unique sequence of human IRTA1-5; and
CC treating a subject having a B cell cancer by administering an anti-IRTA
CC antibody or an antisense oligonucleotide that specifically hybridises to
CC IRTA mRNA so as to prevent overexpression of IRTA protein and hence to
CC arrest cell growth or induce cell death of cancer cells expressing IRTA.
CC The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,
CC multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse
CC large cell lymphoma and follicular lymphoma. The B cell lymphoma is
CC selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-
CC Hodgkin's lymphoma
XX
XX Sequence 592 AA;

Query Match 99.6%; Score 3111; DB 4; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.6e-219;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60
DB 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60
QY 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFFSSASLILQAPLSVFEQDSVV 120
DB 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLNKGAYRCYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLNKGAYRCYKESCCPVSSNT 180
QY 181 VKIQVQBPFPTRPVLRASSFPISGNPVTLCTQLSLERSDVLPRFRFFDDQTLGLWS 240
DB 181 VKIQVQBPFPTRPVLRASSFPISGNPVTLCTQLSLERSDVLPRFRFFDDQTLGLWS 240
QY 181 VKIQVQBPFPTRPVLRASSFPISGNPVTLCTQLSLERSDVLPRFRFFDDQTLGLWS 240
DB 181 VKIQVQBPFPTRPVLRASSFPISGNPVTLCTQLSLERSDVLPRFRFFDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
QY 301 GTRKTLHCETQESLRLTYFYHGVPLRHKSVRCERGASISPSLTENSGNYCTADNG 360
DB 301 GTRKTLHCETQESLRLTYFYHGVPLRHKSVRCERGASISPSLTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPLIYQFHEDAA 420
QY 421 LERRANSAGVAISFLSTAEHSGNYCTADNGFGFQGRSKAVSLSTVPVSHPVLTLSSA 480
DB 421 LERRANSAGVAISFLSTAEHSGNYCTADNGFGFQGRSKAVSLSTVPVSHPVLTLSSA 480
QY 481 EALTTFEGATVTLHCEVQGRSPQLIYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNY 540
DB 481 EALTTFEGATVTLHCEVQGRSPQLIYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSGNY 540
QY 541 CTADNGFGPQRSEVSVLFTVGKQWLASKPKPLAEFLSLTHSFKNLFASSFLP 592
DB 541 CTADNGFGPQRSEVSVLFTVGKQWLASKPKPLAEFLSLTHSFKNLFASSFLP 592

RESULT 2
ADM35236
ID ADM35236 standard; protein; 592 AA.
XX ADM35236;
AC ADM35236;
XX 03-JUN-2004 (first entry)
DE Human LY1448P cancer related protein for cancer detection method.
XX cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX Homo sapiens.
XX WO2003077836-A2.
XX 25-SEP-2003.
XX 06-NOV-2002; 2002WO-US035728.
XX 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX (CORI-) CORIXA CORP.
PA Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
XX Detecting cancer in a patient comprises contacting a biological sample
XX from the patient with a binding agent that binds to a cancer-associated
XX polypeptide and comparing the amount of polypeptide to a predetermined
XX cutoff value.
XX Disclosure; SEQ ID NO 10461; 419pp; English.
XX The invention relates to a method of detecting (M1) cancer in a patient
XX by: (i) contacting a biological sample from the patient with an agent
XX that binds to any of three polypeptides given in the specification; (ii)
XX detecting in a sample an amount of the peptide that binds to the binding
XX agent; and (iii) comparing the amount of polypeptide present in the
XX patient's sample to a predetermined cutoff value. The specification also
XX discloses a separate method for detecting (M2) cancer in a patient by a
XX method similar to M1, except that the detection agent is an
XX oligonucleotide that binds to any of three polynucleotides given in the
XX specification. M1 and M2 are useful for detecting the presence of cancer
XX in a patient, especially chronic lymphocytic leukemia. The applicants
XX have identified specific human polypeptides overexpressed in one or more
XX types of hematological malignancies. This sequence corresponds to a
XX protein used in the method of the invention.
XX Sequence 592 AA;

Query Match 99.6%; Score 3111; DB 7; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.6e-219;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60
DB 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLCKGPRFYSPOKTKWYHR 60
QY 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFFSSASLILQAPLSVFEQDSVV 120
DB 61 YLGEILRETPDNLVEQSEGEYRCQAGSPVHLDFFSSASLILQAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLNKGAYRCYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLPFLNKRTPHIFACLNKGAYRCYKESCCPVSSNT 180
QY 181 VKIQVQBPFPTRPVLRASSFPISGNPVTLCTQLSLERSDVLPRFRFFDDQTLGLWS 240

Db	181	VKIQVQPPTRPVLRASSFPISGNPVTLTCTQLSLERSDVLRRFRFRDQTLGLWS	240
Qy	241	LSPNFQITAMWSKDSGFYWCKAATMHSVILSDSPRSWIQVOIPASHPVLTLSEKALNFE	300
Db	241	LSPNFQITAMWSKDSGFYWCKAATMHSVILSDSPRSWIQVOIPASHPVLTLSEKALNFE	300
Qy	301	GTKVTLHCETQEDSLRLTYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG	360
Db	301	GTKVTLHCETQEDSLRLTYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG	360
Qy	361	LGAKPSKAVSLSVTVPVSHPVNLSPPEDLIPEGAKVTLHCEAQRGLPILYOFHHEDAA	420
Db	361	LGAKPSKAVSLSVTVPVSHPVNLSPPEDLIPEGAKVTLHCEAQRGLPILYOFHHEDAA	420
Qy	421	LERSANSAGGVAISFSLTAEHSGNYCYCTADNGFGPQRSKAVSLISITVPVSHPVLTLSSA	480
Db	421	LERSANSAGGVAISFSLTAEHSGNYCYCTADNGFGPQRSKAVSLISITVPVSHPVLTLSSA	480
Qy	481	EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNY	540
Db	481	EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNY	540
Qy	541	CTADNGFGPQRSVVSILFVTKCKWVLASKPPLAEFSLTHSFKNLFASSFLP	592
Db	541	CTADNGFGPQRSVVSILFVTKCKWVLASHPPLAEFSLTHSFKNLFASSFLP	592
RESULT 3			
Db	AAB82313	AAB82313 standard; protein; 759 AA.	
Ac	AAB82313		
DT	23-JUL-2001	(first entry)	
DE	Human immunoglobulin receptor isoform IRTA2a.		
KW	Immunoglobulin superfamily receptor translocation associated; IRTA;		
KW	IRTA2a; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;		
KW	myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.		
OS	Homo sapiens.		
Key	Location/Qualifiers		
Peptide	1..15	/label= Signal_peptide	
Protein	16..759	/label= Mature_protein	
Modified-site	132..134	/note= "Asn is N-glycosylated"	
Modified-site	383..385	/note= "Asn is N-glycosylated"	
Modified-site	621..623	/note= "Asn is N-glycosylated"	
Modified-site	631..633	/note= "Asn is N-glycosylated"	
Modified-site	714..716	/note= "Asn is N-glycosylated"	
XX	WO200138490-A2.		
PN	31-MAY-2001.		
PF	28-NOV-2000; 2000WO-US032403.		
PR	29-NOV-1999; 99US-0168151P.		
PA	(UYCO) UNIV COLUMBIA NEW YORK.		
PI	Dalla-Tavera R;		
WPI	2001-355921/37..		

DR	N-PSDB; AAF30950.		
XX	New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor		
PT	Translocation Associated proteins, used to treat B cell malignancies		
PT	including lymphomas and multiple myeloma.		
XX	Claim 3; Fig 18B-1-18B-2; 72pp; English.		
XX	The present sequence is that of the novel human immunoglobulin receptor,		
CC	immunoglobulin superfamily receptor translocation associated protein		
CC	isoform 2a (IRTA2a), an Fc receptor involved in the pathogenesis of		
CC	lymphoma and melanoma. Efforts to identify genes involved in chromosomal		
CC	aberrations affecting band 1q21 in multiple myeloma and B cell lymphoma		
CC	led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding		
CC	members of a novel subfamily of related receptors within the		
CC	immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA		
CC	isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82314 and AAB82315).		
CC	IRTA2a is a 759 amino acid secreted glycoprotein with 8 Ig-type domains		
CC	followed by a unique C-terminus. IRTA2b diverges from IRTA2a at residue		
CC	560, extending for a further 32 residues. IRTA2c diverges from IRTA2a at		
CC	residue 746 and extends for a further 231 residues. The IRTA2 genes		
CC	display a specific pattern of expression in mature B cells. IRTA2 is		
CC	expressed in GC centrocytes and in perifollicular cells, which may		
CC	include immunoblasts and memory cells. The invention provides IRTA		
CC	nucleic acids and proteins, and antibodies directed to an epitope of an		
CC	IRTA protein. Methods are claimed for: detecting a B cell malignancy		
CC	comprising a 1q21 chromosomal rearrangement using a nucleic acid molecule		
CC	that specifically hybridises with a unique sequence of human IRTA1-5; and		
CC	treating a subject having a B cell cancer by administering an anti-IRTA		
CC	antibody or an antisense oligonucleotide that specifically hybridises to		
CC	IRTA mRNA so as to prevent overexpression of IRTA protein and hence to		
CC	arrest cell growth or induce cell death of cancer cells expressing IRTA.		
CC	The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma,		
CC	multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse		
CC	large cell lymphoma and follicular lymphoma. The B cell lymphoma is		
CC	selected from mucosa-associated-lymphoid tissue B cell lymphoma or non-		
CC	Hodgkin's lymphoma		
XX	Sequence 759 AA;		
Qy	Query Match 94.4%; Score 2950; DB 4; Length 759;		
Db	Best Local Similarity 98.4%; Pred. No. 3.2e-207;		
Qy	Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;		
Db	1 MLLWVILLVLPVSGGFARTPRPIIFLPQPPWTVTFQGERVTLTKGFRFYSQKTKWYHR	60	
Qy	61 YLQKEILRETDPNILEVQESGYRCOAQGSPLSSPVHLDFSSALILQAPLPSVFEQDSVV	120	
Db	61 YLQKEILRETDPNILEVQESGYRCOAQGSPLSSPVHLDFSSALILQAPLPSVFEQDSVV	120	
Qy	121 LRCRAAEVTLNNTIYKNDNVLAFLNKRDTDFHHPACLDKNGAYRCTGYKSCCPVSSNT	180	
Db	121 LRCRAAEVTLNNTIYKNDNVLAFLNKRDTDFHHPACLDKNGAYRCTGYKSCCPVSSNT	180	
Qy	181 VKIQVQPPTRPVLRASSFPISGNPVTLTCTQLSLERSDVLRRFRFRDQTLGLWS	240	
Db	181 VKIQVQPPTRPVLRASSFPISGNPVTLTCTQLSLERSDVLRRFRFRDQTLGLWS	240	
Qy	241 LSPNFQITAMWSKDSGFYWCKAATMHSVILSDSPRSWIQVOIPASHPVLTLSEKALNFE	300	
Db	241 LSPNFQITAMWSKDSGFYWCKAATMHSVILSDSPRSWIQVOIPASHPVLTLSEKALNFE	300	
Qy	301 GTKVTLHCETQEDSLRLTYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG	360	
Db	301 GTKVTLHCETQEDSLRLTYRFYHEGVPLRHKSVRCERGASISFSLTTENSNGNYCTADNG	360	
Qy	361 LGAKPSKAVSLSVTVPVSHPVNLSPPEDLIPEGAKVTLHCEAQRGLPILYOFHHEDAA	420	
Db	361 LGAKPSKAVSLSVTVPVSHPVNLSPPEDLIPEGAKVTLHCEAQRGLPILYOFHHEDAA	420	
Qy	421 LERSANSAGGVAISFSLTAEHSGNYCYCTADNGFGPQRSKAVSLISITVPVSHPVLTLSSA	480	

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Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVPVSHFVLTLSA 480
Qy 481 BALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNYY 540
Db 481 BALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNYY 540
Qy 541 CTADNGFGPQRSEVVSLFVTGKCWLASKPPL 572
Db 541 CTADNGFGPQRSEVVSLFVT---VPVSRPIL 568

RESULT 4
ADM35235
ID ADM35235 standard; protein; 759 AA.
XX AC
XX ADM35235;
XX DT 03-JUN-2004 (first entry)
XX DE Human LY1448P cancer related protein for cancer detection method.
XX KW cytostatic; T-cell vaccine; detection; cancer;
XX KW chronic lymphocytic leukemia.
XX OS Homo sapiens.
XX PN WO2003077836-A2.
XX PD
XX PF 25-SEP-2003.
XX PR 06-NOV-2002; 2002WO-US035728.
XX PR 06-NOV-2001; 2001US-00040862.
XX PR 23-MAY-2002; 2002US-00154884.
XX PA (CORI-) CORIXA CORP.
XX PI Gaiger A, Algate PA, Mannion J, Retter M;
XX WPI; 2003-756941/71.
XX
XX Detecting cancer in a patient comprises contacting a biological sample
XX from the patient with a binding agent that binds to a cancer-associated
XX polypeptide and comparing the amount of polypeptide to a predetermined
XX cutoff value.
XX
XX Disclosure; SEQ ID NO 10460; 419pp; English.
XX
XX The invention relates to a method of detecting (M1) cancer in a patient
XX by: (i) contacting a biological sample from the patient with an agent
XX that binds to any of three polypeptides given in the specification; (ii)
XX detecting in a sample an amount of the peptide that binds to the binding
XX agent; and (iii) comparing the amount of polypeptide present in the
XX patient's sample to a predetermined cutoff value. The specification also
XX discloses a separate method for detecting (M2) cancer in a patient by a
XX method similar to M1, except that the detection agent is an
XX oligonucleotide that binds to any of three polynucleotides given in the
XX specification. M1 and M2 are useful for detecting the presence of cancer
XX in a patient, especially chronic lymphocytic leukemia. The applicants
XX have identified specific human polypeptides overexpressed in one or more
XX types of hematological malignancies. This sequence corresponds to a
XX protein used in the method of the invention.
XX
XX Sequence 759 AA;
XX
XX Query Match 94.4%; Score 2950; DB 7; Length 759;
XX Best Local Similarity 98.4%; Pred. No. 3.2e-207;
XX Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
XX
XX 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTFQGERVLTCKGFRFYSPOKTKWYH 60
XX 1 MLLWVILLVAPVSGQFARTPRPIIFLQPPWTTFQGERVLTCKGFRFYSPOKTKWYH 60

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Qy 61 YLGKEILRETNDNILEVQSGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVEGDSV 120
Db 61 YLGKEILRETNDNILEVQSGEYRCQAQGSPLSPVHLDFSSASLILQAPLSVEGDSV 120
Qy 121 LRCRAKAVTLNNTIYKNDNLAFLNKRTDPhiPACLKONGAYRCTGYKESCCPVASNT 180
Db 121 LRCRAKAVTLNNTIYKNDNLAFLNKRTDPhiPACLKONGAYRCTGYKESCCPVASNT 180
Qy 181 VKIQVEPFTPRVLRASSFQPIISGNPVTLCETQLSLERSDVPRLRFFRDDQTLGLWS 240
Db 181 VKIQVEPFTPRVLRASSFQPIISGNPVTLCETQLSLERSDVPRLRFFRDDQTLGLWS 240
Qy 241 LSPNFQITAMWSKSGFYWCKAATMPHSVISDSRPMIOVQIPASHVPVLTLSPEKALNFE 300
Db 241 LSPNFQITAMWSKSGFYWCKAATMPHSVISDSRPMIOVQIPASHVPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLRYFVHEGVPLRHKSVCERGASISFSLTTENSGNYICTADNG 360
Db 301 GTKVTLHCETOEDSLRTLRYFVHEGVPLRHKSVCERGASISFSLTTENSGNYICTADNG 360
Qy 361 LGAKPSKAVLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVLSVTPVSHPVNLSSPDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVPVSHFVLTLSA 480
Db 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVLSITVPVSHFVLTLSA 480
Qy 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNYY 540
Db 481 EALTPEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTGHSGNYY 540
Qy 541 CTADNGFGPQRSEVVSLFVTGKCWLASKPPL 572
Db 541 CTADNGFGPQRSEVVSLFVT---VPVSRPIL 568

RESULT 5
AAB82315
ID AAB82315 standard; protein; 977 AA.
XX AC
XX AAB82315;
XX DT 23-JUL-2001 (first entry)
XX DE Human immunoglobulin receptor isoform INTA2c.
XX
XX Immunoglobulin superfamily receptor translocation associated; IRTA;
XX IRTA2c; human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma;
XX myeloma; B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..15
XX Protein 16..977
XX Modified-site /label= Mature_protein
XX Modified-site /label= Mature_protein
XX Modified-site /note= "Asn is N-glycosylated"
XX Modified-site 383..385
XX Modified-site /note= "Asn is N-glycosylated"
XX Modified-site 621..623
XX Modified-site /note= "Asn is N-glycosylated"
XX Modified-site 631..633
XX Modified-site /note= "Asn is N-glycosylated"
XX Modified-site 714..716
XX Modified-site /note= "Asn is N-glycosylated"
XX Modified-site 795..797
XX Modified-site /note= "Asn is N-glycosylated"
XX Modified-site 806..808
XX Modified-site /note= "Asn is N-glycosylated"

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FT	Modified-site	816..818 /note= "Asn is N-glycosylated"
FT	Modified-site	843...845 /note= "Asn is N-glycosylated"
FT	Domain	851...873 /note= "transmembrane domain"
FT	Binding-site	899...902 /note= "putative consensus Src-homology 2 (SH2) binding domain"
FT	Binding-site	924...927 /note= "putative consensus Src-homology 2 (SH2) binding domain"
FT	Binding-site	954...957 /note= "putative consensus Src-homology 2 (SH2) binding domain"
WO	200138490-A2.	
XX	31-MAY-2001.	
XX	28-NOV-2000; 200OWO-US0322403.	
XX	29-NOV-1999; 99US-0168151P.	
PR	(UYCO) UNIV COLUMBIA NEW YORK.	
PA	Dalla-Favera R;	
PI	WPI; 2001-355921/37.	
DR	N-PSDB; AAF30952.	
XX	New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor Translocation Associated proteins, used to treat B cell malignancies including lymphomas and multiple myeloma.	
XX	Claim 3; Fig 1B-1-1B-2; 72pp; English.	
XX	The present sequence is that of the novel human immunoglobulin receptor, immunoglobulin superfamily receptor translocation associated protein isoform 2c (IRTA2c), an FC receptor involved in the pathogenesis of lymphoma and melanoma. Efforts to identify genes involved in chromosomal aberrations affecting band Igk2l in multiple myeloma and B cell lymphoma led to the discovery of IRTA2 and IRTA1 (see AAB82312) as founding members of a novel subfamily of related receptors within the immunoreceptor family. The IRTA2 locus is transcribed into 3 major mRNA isoforms, IRTA2a, IRTA2b and IRTA2c (see also AAB82313 and AAB82314). IRTA2c is the longest isoform. It is a type I transmembrane glycoprotein. Each SH2 binding site agrees with the immune receptor tyrosine-based inhibition motif (ITIM) consensus and is encoded by a separate exon. The IRTA genes display a specific pattern of expression in mature B cells. IRTA2 is expressed in GC centrocytes and in perifollicular cells, which may include immunoblasts and memory cells. The invention provides IRTA nucleic acids and proteins, and antibodies directed to epitopes of IRTA proteins. Methods are claimed for: detecting a B cell malignancy comprising a Igk2l chromosomal rearrangement using a nucleic acid molecule that specifically hybridises with a unique sequence of human IRTA1-5; and treating a subject having a B cell cancer by administering an anti-IRTA antibody or an antisense oligonucleotide that specifically hybridises to IRTA mRNA so as to prevent overexpression of IRTA protein and hence to arrest cell growth or induce cell death of cancer cells expressing IRTA. The B cell cancer is selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma, Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma and follicular lymphoma. The B cell lymphoma is Hodgkin's lymphoma	
XX	Sequence 977 AA;	
XX	Query Match 94.4%; Score 2950; DB 4; Length 977;	
XX	Best Local Similarity 98.4%; Pred. No. 4.4e-207;	
XX	Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;	
OY	1 MLHWILLVLAVSGQFARTPRPIIFLOPPWTTFQGERVTLTCKGRFFSPQKTKWYHR 60	

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XX WPI; 2003-354551/33.
DR N-PSDB; ACC49533.
XX
XX New antibodies against tumor-associated antigenic target polypeptide,
XX useful for treating or diagnosing tumors or cancers in mammals, e.g.
XX prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
XX carcinomas.
XX
XX Claim 2; Fig 97; 285pp; English.
XX
XX ACC49493 to ACC49552 encode the human tumour-associated antigenic target
XX (TAT) proteins given in ABP97175 to ABP97234. The present invention
XX describes an isolated antibody that binds to a polypeptide having at
XX least 80 % sequence identity to any of the 60 150-800 residue amino acid
XX sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
XX its associated signal peptide, encoded by any of the 60 2000-3000 base
XX pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have
XX cytostatic activity. The antibody can be used for treating or diagnosing
XX tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
XX cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
XX cell carcinomas, or thyroid cancer
XX
XX Sequence 977 AA;
SQ

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Query Match 94.4%; Score 2950; DB 6; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.4e-207;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
QY 61 YLGEILRETPDNILEVQESGEYRCQAGSPVHLDFFSSASLILQAPLSVEGDSVV 120
DB 61 YLGEILRETPDNILEVQESGEYRCQAGSPVHLDFFSSASLILQAPLSVEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPVLRFFRDDQTLGLGWS 240
DB 181 VKIQVEPFPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPVLRFFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVPSHPVNLNLSPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPVLTLSA 480
DB 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLSVTVPSHPVLTLSA 480
QY 481 EALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
DB 481 EALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNGYY 540
QY 541 CTADNGFGPQRSSEVSVLFTVTKCWMVLASKPPL 572
DB 541 CTADNGFGPQRSSEVSVLFTVTKCWMVLASKPPL 572

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XX ADM35237;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human LY1448P cancer related protein for cancer detection method.
XX
XX cytostatic; T-cell vaccine; detection; cancer;
XX chronic lymphocytic leukemia.
XX
XX Homo sapiens.
XX
XX WO2003077836-A2.
XX
XX 25-SEP-2003.
XX
XX 06-NOV-2002; 2002WO-US035728.
XX
XX 06-NOV-2001; 2001US-00040862.
XX
XX 23-MAY-2002; 2002US-00154884.
XX
XX (CORI-) CORIXA CORP.
XX
XX Gaiger A, Algate PA, Mannion J, Retter M;
XX
XX WPI; 2003-756941/71.
XX
XX Detecting cancer in a patient comprises contacting a biological sample
XX from the patient with a binding agent that binds to a cancer-associated
XX polypeptide and comparing the amount of polypeptide to a predetermined
XX cutoff value.
XX
XX Disclosure; SEQ ID NO 10462; 419pp; English.
XX
XX The invention relates to a method of detecting (M1) cancer in a patient
XX by: (i) contacting a biological sample from the patient with an agent
XX that binds to any of three polypeptides given in the specification; (ii)
XX detecting in a sample an amount of the peptide that binds to the binding
XX agent; and (iii) comparing the amount of polypeptide present in the
XX patient's sample to a predetermined cutoff value. The specification also
XX discloses a separate method for detecting (M2) cancer in a patient by a
XX method similar to M1, except that the detection agent is an
XX oligonucleotide that binds to any of three polynucleotides given in the
XX specification. M1 and M2 are useful for detecting the presence of cancer
XX in a patient, especially chronic lymphocytic leukemia. The applicants
XX have identified specific human polypeptides overexpressed in one or more
XX types of hematological malignancies. This sequence corresponds to a
XX protein used in the method of the invention.
XX
XX Sequence 977 AA;

```

```

Query Match 94.4%; Score 2950; DB 7; Length 977;
Best Local Similarity 98.4%; Pred. No. 4.4e-207;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOKTKWYHR 60
QY 61 YLGEILRETPDNILEVQESGEYRCQAGSPVHLDFFSSASLILQAPLSVEGDSVV 120
DB 61 YLGEILRETPDNILEVQESGEYRCQAGSPVHLDFFSSASLILQAPLSVEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPFPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPVLRFFRDDQTLGLGWS 240
DB 181 VKIQVEPFPTRPVLRASSFPQISGNPVTLCETQLSLERSDVPVLRFFRDDQTLGLGWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOQIPASHPVLTLSPEKALNFE 300

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Db 241 LSNFQITAMWSKDSGYWYKAAATMPHSVLSDSFRSHIQVOIPASHPVLTLSPEKALNFE 300
Qy 301 GTKVTLHCETQEDSLRLTYRFFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360
Db 301 GTKVTLHCETQEDSLRLTYRFFYHEGVPLRHKSVCRCGASISFSLTTTNSGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFSGAKVTLHCCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSPPEDLIFSGAKVTLHCCEAQRGSLPILYQFHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLISITVPVSHVPLTLSSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQRSKAVSLISITVPVSHVPLTLSSA 480
Qy 481 EALTPEGATVTLHCCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTTEGHSGNYY 540
Db 481 EALTPEGATVTLHCCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSPFSLTTEGHSGNYY 540
Qy 541 CTADNGFGPQRSSEVVSFLVTGKCVWLASKPPL 572
Db 541 CTADNGFGPQRSSEVVSFLVTGKCVWLASKPPL 572
RESULT 8
ID ABU99155 standard; protein; 582 AA.
XX AC ABU99155;
XX XX
DT 01-AUG-2003 (first entry)
XX XX
DE Novel human GPCR related protein NOV17a.
XX Human; G-protein coupled receptor related protein; GPCR related protein;
KW NOV; cytostatic; cardiant; antiarteriosclerotic; antidiabetic;
KW immunomodulator; anti-HIV; anorectic; antilasthmatic; haemostatic;
KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;
KW diabetes; immune disorder; AIDS; obesity; asthma;
KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;
KW infection; multiple sclerosis; cancer-associated cachexia;
KW wasting disorder; chronic disease; neurogenesis; cell differentiation;
KW cell proliferation; haematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.
XX OS Homo sapiens.
XX XX
XX WO200299116-A2.
XX PD 12-DEC-2002.
XX XX
XX 04-JUN-2002; 2002WO-US017428.
XX PF
XX PR 04-JUN-2001; 2001US-0295607P.
XX PR 04-JUN-2001; 2001US-0295664P.
XX PR 06-JUN-2001; 2001US-0296404P.
XX PR 06-JUN-2001; 2001US-0296418P.
XX PR 14-JUN-2001; 2001US-0296285P.
XX PR 15-JUN-2001; 2001US-0298556P.
XX PR 21-JUN-2001; 2001US-029949P.
XX PR 26-JUN-2001; 2001US-0300883P.
XX PR 28-JUN-2001; 2001US-0301550P.
XX PR 13-AUG-2001; 2001US-0311972P.
XX PR 27-AUG-2001; 2001US-0315071P.
XX PR 29-AUG-2001; 2001US-0315660P.
XX PR 14-SEP-2001; 2001US-0322293P.
XX PR 17-SEP-2001; 2001US-0322706P.
XX PR 14-DEC-2001; 2001US-0341186P.
XX PR 28-FEB-2002; 2002US-0361189P.
XX PR 12-MAR-2002; 2002US-0363673P.
XX PR 12-MAR-2002; 2002US-0363676P.
XX PR 03-JUN-2002; 2002US-00363676.

PA (CURA-) CURAGEN CORP.
XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR;
PI Gangoli EA, Gerlach VL, Gorman L, Guo X, Hjalte T, Kekuda R, Li L;
PI MacDougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M; M;
PI Pena CE, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CM;
PI Voss EZ, Zerhusen BD;
XX WPI: 2003-140627/13.
DR N-PSDB; ACD03659.
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX Claim 1; Page 166; 332pp; English.
XX The invention describes an isolated polypeptide (I) comprising any of 27
CC 118-961 residue amino acid sequences, given in the specification, a
CC mature form of them, a sequence that is at least 95 % identical to them,
CC or a sequence having one or more conservative substitutions in them. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease selected from a pathology
CC associated with the polypeptide. The NOVX polypeptides, polynucleotides
CC and antibodies are useful in treating or preventing NOVX-associated
CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune
CC disease, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's
CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-
CC associated cachexia, and other wasting disorders associated with chronic
CC diseases. The nucleic acids and polypeptides may also be used as targets
CC for the identification of small molecules that modulate or inhibit e.g.
CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,
CC wound healing and angiogenesis, in gene therapy, in generation of
CC antibodies that bind immunospecifically to NOVX substances for use in
CC therapeutic or diagnostic methods. The nucleic acids are further used as
CC hybridisation probes in chromosome mapping, tissue typing, preventive
CC medicine, and pharmacogenomics. The polypeptides are also useful as
CC vaccines. This is the amino acid sequence of a novel human G-protein
CC coupled receptor related protein NOV
XX Sequence 582 AA;
Query Match 38.2%; Score 1193.5; DB 6; Length 582;
Best Local Similarity 45.5%; Pred. No. 1.1e-78;
Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;
Qy 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCGFRFYSQ-KTKWTH 59
Db 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCGFRFYSQ-KTKWTH 59
Qy 60 RYLGKILRETDPNILEVQESGEYRCQAGSPLSSPVHLDFSSASILCAPLSVPEGDSV 119
Db 60 RYLGKILRETDPNILEVQESGEYRCQAGSPLSSPVHLDFSSASILCAPLSVPEGDSV 119
Qy 61 ---DEKLLIKKHDKI-QITEPGNYQCKTRGSSLSDAHVHVEFDPDWILLQALHPVEGDNV 116
Db 61 ---DEKLLIKKHDKI-QITEPGNYQCKTRGSSLSDAHVHVEFDPDWILLQALHPVEGDNV 116
Qy 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHICHLKNDGAYRCTGYKESC---CPV 176
Db 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHICHLKNDGAYRCTGYKESC---CPV 176
Qy 117 ILRCQKDKNKHVTHQYKDKGKQLPNSYNLEKITVNSVRDNSKYHCTAYRKYDIEV 176
Db 117 ILRCQKDKNKHVTHQYKDKGKQLPNSYNLEKITVNSVRDNSKYHCTAYRKYDIEV 176
Qy 177 SSNTVKIQVQEPTRPVRPLRASSPQI-SGNPVTLTCTQLSLERSDYPLRFRPDDDTGLG 236
Db 177 SSNTVKIQVQEPTRPVRPLRASSPQI-SGNPVTLTCTQLSLERSDYPLRFRPDDDTGLG 236
Qy 177 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTITCTQLSPQRPDVOLOFSLFRDQTGLG 236
Db 177 TSKPLNIQVQELFLHPVLRASSSTPIEGSPMTITCTQLSPQRPDVOLOFSLFRDQTGLG 236
Qy 237 LKWSLSNFOITAMWSKDSGYWYKAAATMPHSVLSDSFRSHIQVOIPASHPVLTLSPEK 295
Db 237 LKWSLSNFOITAMWSKDSGYWYKAAATMPHSVLSDSFRSHIQVOIPASHPVLTLSPEK 295
Qy 237 LGWSRSPRLQIPAMWTEDSGSYVCEVETVTHSKKSLRSQIRVQRPVSNVLEIRPTG 296
Db 237 LGWSRSPRLQIPAMWTEDSGSYVCEVETVTHSKKSLRSQIRVQRPVSNVLEIRPTG 296
Qy 296 ALNPEGTKVTLHCETQEDSLRLTYRFFYHEGVPLRHKSVCRCGASISFSLTT---ENSGN 352
Db 296 ALNPEGTKVTLHCETQEDSLRLTYRFFYHEGVPLRHKSVCRCGASISFSLTT---ENSGN 352
Qy 297 GQLIEGENMVLCISVAQSGTGTFSMHKEG-RVRSIGRKTQRSILAEHLVLTVKESDAGR 355
Db 297 GQLIEGENMVLCISVAQSGTGTFSMHKEG-RVRSIGRKTQRSILAEHLVLTVKESDAGR 355
Qy 353 YYCTADNGLGAKSKAVSLSVTPVSHVPLNLSPPEDLIFSGAKVTLHCCEAQRGSLPILY 412
Db 353 YYCTADNGLGAKSKAVSLSVTPVSHVPLNLSPPEDLIFSGAKVTLHCCEAQRGSLPILY 412

Db 356 YYCAADNVHSPILSTWIRTVRI PVSHPVLTFRAPRAHTVVGDLELHCBLSRGSPILY 415
 QY 413 QFHEDAAALERSANSAGVAISLSLTAHSGNYCTADNGFGPQORSKAVSLITVPVSH 472
 Db 416 RYFHEDEVTLGNSSAPSGGASFNLSLTAHSGNYSCDADNGLGAQHSHGSLRVTVFVSR 475
 QY 473 PVLTLSSAEALTFFGATVTLHCEVQSGSPQILYQFYHEDNPLVSSSTPSVGRVSFSPSLT 532
 Db 476 PVLTLRPGAQAVGDLELHCBLSRGSPILYQFYHEDDNLGNISAHSGGASFNLSLT 535
 QY 533 EHGSGNYCTADNGFGPQORSVSLFVTG 561
 Db 536 TEHSGNYSCEADNGLGAQHSKVVTLNVTG 564

RESULT 9

ADM93875
 ID ADM93875 standard; protein; 582 AA.

XX AC ADM93875;

XX DT 17-JUN-2004 (first entry)

XX DE Human NOV protein #47.

XX KW gene therapy; vaccine; NOVX; cancer; neurodegenerative disorder;
 KW Parkinson's disease; metabolic disorder; diabetes; obesity;
 KW immune related disorder; tissue typing; human.

XX OS Homo sapiens.

XX FN US2004009480-A1.

XX PD 15-JAN-2004.

XX PF 03-JUN-2002; 2002US-00162335.

XX PR 04-JUN-2001; 2001US-0295607P.

XX PR 04-JUN-2001; 2001US-0295661P.

XX PR 06-JUN-2001; 2001US-0296404P.

XX PR 06-JUN-2001; 2001US-0296418P.

XX PR 11-JUN-2001; 2001US-0297414P.

XX PR 12-JUN-2001; 2001US-0297567P.

XX PR 14-JUN-2001; 2001US-0298285P.

XX PR 15-JUN-2001; 2001US-0298556P.

XX PR 21-JUN-2001; 2001US-0299499P.

XX PR 26-JUN-2001; 2001US-0300883P.

XX PR 28-JUN-2001; 2001US-0301550P.

XX PR 13-AUG-2001; 2001US-0311972P.

XX PR 27-AUG-2001; 2001US-0315069P.

XX PR 27-AUG-2001; 2001US-0315071P.

XX PR 29-AUG-2001; 2001US-0315660P.

XX PR 17-SEP-2001; 2001US-0322706P.

XX PR 14-DEC-2001; 2001US-0341186P.

XX PR 28-FEB-2002; 2002US-0361189P.

XX PR 12-MAR-2002; 2002US-0363673P.

XX PR 12-MAR-2002; 2002US-0363676P.

XX (ANDE//) ANDERSON D W.

XX (BAUM//) BAUMGARTNER J C.

XX (BOLD//) BOLDOG F L.

XX (CASM//) CASMAN S J.

XX (EDIN//) EDINGER S R.

XX (GANG//) GANGOLLI E A.

XX (GERL//) GERLACH V.

XX (GORM//) GORMAN L.

XX (GUOX//) GUO X S.

XX (HJAL//) HJALT T.

XX (KEKU//) KEKUDA R.

XX (LILL//) LI L.

XX (MACD//) MACDOUGALL J R.

XX (MALY//) MALYANKAR U M.

PA (MILL//) MILLET I.
 PA (PADI//) PADIGARU M.
 PA (PATI//) PATTURAJAN M.
 PA (PENA//) PENA C E A.
 PA (RAST//) RASTELLI L.
 PA (SHIM//) SHIMKETS R A.
 PA (STON//) STONE D J.
 PA (SPYT//) SPYTEK K A.
 PA (VERN//) VERNET C A M.
 PA (VOSS//) VOSS E Z.
 PA (ZERH//) ZERHUSEN B D.
 XX
 XX Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR,
 PI Gangolli EA, Gerlach V, Gorman L, Guo XS, Hjal T, Kekuda R, Li L,
 PI MacDougall JR, Malyankar UM, Millet I, Padigaru M, Paturajan M,
 PI Pena CE, Rastelli L, Shimkets RA, Stone DJ, Spytek KA, Vernet CM,
 PI Voss EZ, Zerhusen BD;
 XX WPI; 2004-090456/09.
 DR N-PSDB; ADM93874.
 XX
 XX New NOVX polypeptide, useful for preparing a composition for treating or
 PT preventing e.g., cancer, neurodegenerative disorders such as Parkinson's
 PT disease, or metabolic disorders such as diabetes or obesity, or for
 PT tissue typing.
 XX
 XX Claim 1; SEQ ID NO 94; 202pp; English.
 XX
 XX The invention relates to an isolated NOVX polypeptide. The polypeptide is
 CC useful for preparing a composition for treating or preventing a pathology
 CC associated with NOVX polypeptide e.g. cancer, neurodegenerative disorders
 CC such as Parkinson's disease, metabolic disorders such as diabetes or
 CC obesity or immune related disorders or for tissue typing. The present
 CC sequence represents a human NOV protein.
 XX
 XX Sequence 582 AA;

Query Match 38.2%; Score 1193.5; DB 8; Length 582;
 Best Local Similarity 45.5%; Pred. No. 1.1e-78;
 Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;
 QY 1 MLLAVILLVLPVSGQFARTPRPIIFLPQWTTVFQSERVTLTCKGFRFYSPQ-KTWYH 59
 Db 1 MLLWLLILLITPGEQSGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDITYW 60
 QY 60 RYLKHEILRETPDNILEVOESGEYRCQAQSPSPVHLPDFSSASLIQAPLSVFEGDSV 119
 Db 61 ---DEKLLKIKHDKI-QITEFGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFE 116
 QY 120 VLRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFHPACLKDNAGYRGTGYKESC---CPV 176
 Db 117 ILRCQKDNKTHOKVYKDGKQLPNSVLEKIVNSVRDNRKXHTARKFILLIEV 176
 QY 177 SSNTVKIQVQEPTRPVLRASSFPISGNPVTLTCTQLSLERSDVPFLRFRFFDDQTLG 236
 Db 177 TSKPLNIQVQLFLHPVLRASSTPIEGSPMTLTCTQLSPQRPDVQLQSFSLFRDQTLG 236
 QY 237 LGWSLSNFOITAMKSKDSGYWCKAATMPHSVTSDSPRWIQVQ-IPASHVPLTLPSEK 295
 Db 237 LGWSRSPRLQIPAMWTEDSGVSWEVETVTHSIKRSQRQIRVQRPVSNVNLEIRPTG 296
 QY 296 ALNFEGRKTVLHCETQBDLSLTLYRFYHGEVPLRHKSVRCERGASISFSLT---ENSGN 352
 Db 297 GQLIEGENWVLICVAQSGGTVTFTSWHKEG-RVRSLSGRKTRSLAELHVLTVKESDAGR 355
 QY 353 YYCTADNGLGAKPSKAVSLVTVVPSHPVLNLSPEDLIFEGAKVTLHCAQSGSLDILY 412
 Db 356 YYCAADNVHSPILSTWIRTVRI PVSHPVLTFRAPRAHTVVGDLELHCBLSRGSPILY 415
 QY 413 QFHEDAAALERSANSAGVAISLSLTAHSGNYCTADNGFGPQORSKAVSLITVPVSH 472
 Db 416 RYFHEDEVTLGNSSAPSGGASFNLSLTAHSGNYSCDADNGLGAQHSHGSLRVTVFVSR 475

QY 473 PVLTLSSAEALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPVGVRVSFSLT 532
Db 476 PVLTLRPAQAQAVGVGDLLEHCESLRGSPFIYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EGHSGNYCTADNGFGPQSEVVSFLVTG 561
Db 536 TEHSGNYCEADNGLGAQHSKVTLNVTG 564

RESULT 10
ID ADM06089 standard; protein; 707 AA.
XX
AC ADM06089;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:4774.
XX
KW human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
XX
PN EPI347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (RPAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM03646.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 4774; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 707 AA;

Query Match 38.2%; Score 1193.5; DB 7; Length 707;
Best Local Similarity 45.5%; Pred. No. 1.5e-78;
Matches 259; Conservative 76; Mismatches 22; Indels 13; Gaps 7;
QY 1 MLLWVLLVLPVSGQFARTPRPIIFLPQMTTTFQGERVLTCKGFFYSQ-KTKWYH 59
Db 1 MLLWVLLVLTGREGSGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDYVYH 60
QY 60 RVLGHEILRETPDNLVEQSEYRCQAGSPVHLDPSASLILOAPLSYFEGDSV 119
Db 61 ---DBKLKIKHDKI-QTEPGNYQCKRGSSLDVHVEFSPDWLILOALHPFEGDNV 116
QY 120 VLRCRAKAEVTLNNTYIKNDNLVFLNKTDFPHIACLKONGAYRCTGYKESC---CPV 176

Db 117 ILRCGGKDNKNTKQVYKDGKQLPNSYNLEKITVNSVRDNSKYHCTAYRKFYILDIEV 176
QY 177 SSNTVKIQVQPPFRPVLIRASSFQPISGNPVTLTCTQLSILERSDVLRRFRFRDDOTLG 236
Db 177 TSKPLNTQVQELFLHPVLRASSSTPIEGSPMTLTCETQLSPQPDVQLQSLFRDSQTLG 236
QY 237 LGWSLSPNFQITAMWSKDSGFYWCKAATMPHSVISDSRPMIOVQ-IPASHPVLTLSPEK 295
Db 237 LGWSRSPKLQIPANWTEDSGSYWCVEVTVTHSIKKRSILRSQIRVQRPVPSNVNLEIRPTG 296
QY 296 ALNFEPTKVTLHCETOEDSLRTLYRFYHEGVPLRHKSVRCERGASISFSLT---ENSGN 352
Db 297 GQLIEGENNVLICVAQSGGTVTFSWKEG-RVRSGLRKTQSRLLAEHLVLTVESDAGR 355
QY 353 YYCTADNGLGAKPKSKAVSLSVTPVSHPVNLNLPEDLIFEGAKVTLHCEAQRGSLPILY 412
Db 356 YYCAADNVHSPILSTWIRVTVRIPVSHPVLTFRAPRAHTVVGDLLEHCESLRGSPPIY 415
QY 413 QPHHEDAALERRSANSAGVAISFSLTAHSGNYCTADNGFGPQSEVVSFLVTG 472
Db 416 RPYHEDVTLGNSSAPSGGGASFNLSLTAHSGNYSCDADNGLGAQHSGLVSLRVTPVSR 475
QY 473 PVLTLSSAEALTFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPVGVRVSFSLT 532
Db 476 PVLTLRPAQAQAVGVGDLLEHCESLRGSPFIYWFYHEDDTLGNISAHSGGASFNLSLT 535
QY 533 EGHSGNYCTADNGFGPQSEVVSFLVTG 561
Db 536 TEHSGNYCEADNGLGAQHSKVTLNVTG 564

RESULT 11
ID AAB82316 standard; protein; 734 AA.
XX
AC AAB82316;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human immunoglobulin receptor IRTA3 protein.
XX
KW Immunoglobulin superfamily receptor translocation associated; IRTA3;
KW human; immunoglobulin receptor; Fc receptor; melanoma; lymphoma; myeloma;
KW B cell malignancy; cancer; chromosome 1q21; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200138490-A2.
XX
PD 31-MAY-2001.
XX
PF 28-NOV-2000; 2000WO-US032403.
XX
PR 29-NOV-1999; 99US-0168151P.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Dalla-Favera R;
XX
DR WPI; 2001-355921/37.
DR N-PSDB; AAF30953.
XX
PT New genes encoding immunoglobulin receptor, Immunoglobulin super Receptor
PT Translocation Associated proteins, used to treat B cell malignancies
PT including lymphomas and multiple myeloma.
XX
PS Claim 4; Fig 18C-1-18C-2; 72pp; English.
XX
CC The present sequence is that of the novel human immunoglobulin receptor,
CC immunoglobulin superfamily receptor translocation associated protein 3
CC (IRTA3), an Fc receptor involved in the pathogenesis of lymphoma and
CC melanoma. Efforts to identify genes involved in chromosomal aberrations
CC affecting band 1q21 in multiple myeloma and B cell lymphoma led to the

CC discovery of IRTA1 and IRTA2 (see AAB82312-15) as founding members of a
 CC novel subfamily of related receptors within the immunoreceptor family. 3
 CC Additional proteins, IRTA3, IRTA4 and IRTA5 (see AAB82316-18), were
 CC subsequently identified, which are also members of this novel subfamily.
 CC The IRTA genes display a specific pattern of expression in mature B
 CC cells. IRTA3 is expressed in GC centrocytes and in perifollicular cells,
 CC which may include lymphoblasts and memory cells. This is analogous to
 CC IRTA2 expression. The invention provides IRTA nucleic acids and proteins,
 CC and antibodies directed to an epitope of an IRTA protein. Methods are
 CC claimed for: detecting a B cell malignancy comprising a Ig21 chromosomal
 CC rearrangement using a nucleic acid molecule that specifically hybridises
 CC with a unique sequence of human IRTA1-5; and treating a subject having a
 CC B cell cancer by administering an anti-IRTA antibody or an antisense
 CC oligonucleotide that specifically hybridises to IRTA mRNA so as to
 CC prevent overexpression of IRTA protein and hence to arrest cell growth or
 CC induce cell death of cancer cells expressing IRTA. The B cell cancer is
 CC selected from B cell lymphoma, mantle cell lymphoma, multiple myeloma,
 CC Burkitt's lymphoma, marginal zone lymphoma, diffuse large cell lymphoma
 CC and follicular lymphoma. The B cell lymphoma is selected from mucosa-
 CC associated-lymphoid tissue B cell lymphoma or non-Hodgkin's lymphoma
 CC XX
 SQ Sequence 734 AA;

Query Match 38.2%; Score 1193.5; DB 4; Length 734;
 Best Local Similarity 45.5%; Pred. No. 1.5e-78;
 Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPO-KTKWYH 59
 DB 1 MLLWLLILLTPGREGQGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDYVYH 60

QY 60 RYLCKEILRETPDNLIVQSGEYRCQAQSPSSPVHLDFFSASILLQAPLSVFEGDSV 119
 DB 61 ---DEKLLIKHDKI-QITEFGNYQCKTRGSSLSDAVHVEFSDWLLILQALHPFEGDNV 116

QY 120 VLRCRAAEVTLNNTIYKNDNLVAFNLKRTDFHPIHACLKNDGAYRCTGKYESC---CPV 176
 DB 117 ILRCQKDNKNTQKVVYKDGKQLPNSYNLEKITVNSVSRDNSKYHCTAYRKFIYLDIEV 176

QY 177 SSNTVKIQVQEPFTRPVLRASSQPTISGNPVTLTCETQLSLERSDVLPRFRDDOTLG 236
 DB 177 TSKPLNIQVQLFLHPVLRASSSTPIEGSPMTLTCETQLSPQPDVQLQSLFRDSOTLG 236

QY 237 LGWLSLSPNFOITAWMSKDSGFYCKAATMPHSVLSDSPSRWIOVQ-IPASHPVLTLSPEK 295
 DB 237 LGWRSRPLQIPAMWTEDSGSYCEVETVTHSIKKSRLRSQIRVQVPSVNVNLEIRPTG 296

QY 296 ALNFEQTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVRCERGASISFSLTT---ENSGN 352
 DB 297 GQLTEGENMYLVICSVAQSGGVTFVSMHKEG-RVRSGLRKTQRLSLLAELHVLTVKESDAGR 355

QY 353 YVCTADNGLGAKSPKAVSLVTVVSHVPLNLSPEDLIPFGAKVTLHCEAQRGSLPIILY 412
 DB 356 YVCAADNVHSPILSTVTRVTRIPVSHPVLTFRAPRAHTVVGDLLEHCELSRGSPPILY 415

QY 413 QFHEDAAALRRSANSAGGVAISFSLTAHSGNYYCTADNGFQQRKAVSLISITVPVSH 472
 DB 416 RFYHEDVTLGNSSAPSGGASFNLSLTAHSGNYSADADNGLGAQSHGVSRLRVTPVSR 475

QY 473 PVLTLSABALTEGATVTLHCEVQRGSPQIILYQFTHEDMPLVSSSTPVGVRVSFSLT 532
 DB 476 PVLTLPAPGAQVAVGDDLELHCELSRGSPPILYFYFHYHEDDTLGNISAHSGGASFNLSLT 535

QY 533 EGHSGNYCTADNGFGQRSEVWSLFTVG 561
 DB 536 TERHSGNYSCEADNGLGQHSKVTNLNTVG 564

RESULT 12
 ADM35238
 ID ADM35238 standard; protein; 734 AA.
 XX
 AC ADM35238;

XX 03-JUN-2004 (first entry)
 XX Human LY1448P cancer related protein for cancer detection method.
 DE cytostatic; T-cell vaccine; detection; cancer;
 KW chronic lymphocytic leukemia.
 XX Homo sapiens.
 XX WO2003077836-A2.
 XX 25-SEP-2003.
 XX 06-NOV-2002; 2002WO-US035728.
 PR 06-NOV-2001; 2001US-00040962.
 PR 23-MAY-2002; 2002US-00154884.
 PA (CORI-) CORIXA CORP.
 XX Gaiger A, Algate PA, Mannion J, Retter M;
 XX WPI; 2003-756941/71.
 DR Detecting cancer in a patient comprises contacting a biological sample
 XX from the patient with a binding agent that binds to a cancer-associated
 PT polypeptide and comparing the amount of polypeptide to a predetermined
 PT cutoff value.
 XX Disclosure; SEQ ID NO 10463; 419pp; English.
 XX The invention relates to a method of detecting (M1) cancer in a patient
 CC by: (i) contacting a biological sample from the patient with an agent
 CC that binds to any of three polypeptides given in the specification; (ii)
 CC detecting in a sample an amount of the peptide that binds to the binding
 CC agent; and (iii) comparing the amount of polypeptide present in the
 CC patient's sample to a predetermined cutoff value. The specification also
 CC discloses a separate method for detecting (M2) cancer in a patient by a
 CC method similar to M1, except that the detection agent is an
 CC oligonucleotide that binds to any of three polynucleotides given in the
 CC specification. M1 and M2 are useful for detecting the presence of cancer
 CC in a patient, especially chronic lymphocytic leukemia. The applicants
 CC have identified specific human polypeptides overexpressed in one or more
 CC types of hematological malignancies. This sequence corresponds to a
 CC protein used in the method of the invention.
 XX Sequence 734 AA;

Query Match 38.2%; Score 1193.5; DB 7; Length 734;
 Best Local Similarity 45.5%; Pred. No. 1.5e-78;
 Matches 259; Conservative 76; Mismatches 221; Indels 13; Gaps 7;

QY 1 MLLWVILLVLPVSGQPARTPRPIIFLOPPWTVFQGERVTLCKGFRFYSPO-KTKWYH 59
 DB 1 MLLWLLILLTPGREGQGVAPKAVLLNPPWSTAFKGEKVALICSSISHSLAQGDYVYH 60

QY 60 RYLCKEILRETPDNLIVQSGEYRCQAQSPSSPVHLDFFSASILLQAPLSVFEGDSV 119
 DB 61 ---DEKLLIKHDKI-QITEFGNYQCKTRGSSLSDAVHVEFSDWLLILQALHPFEGDNV 116

QY 120 VLRCRAAEVTLNNTIYKNDNLVAFNLKRTDFHPIHACLKNDGAYRCTGKYESC---CPV 176
 DB 117 ILRCQKDNKNTQKVVYKDGKQLPNSYNLEKITVNSVSRDNSKYHCTAYRKFIYLDIEV 176

QY 177 SSNTVKIQVQEPFTRPVLRASSQPTISGNPVTLTCETQLSLERSDVLPRFRDDOTLG 236
 DB 177 TSKPLNIQVQLFLHPVLRASSSTPIEGSPMTLTCETQLSPQPDVQLQSLFRDSOTLG 236

QY 237 LGWLSLSPNFOITAWMSKDSGFYCKAATMPHSVLSDSPSRWIOVQ-IPASHPVLTLSPEK 295
 DB 237 LGWRSRPLQIPAMWTEDSGSYCEVETVTHSIKKSRLRSQIRVQVPSVNVNLEIRPTG 296

QY 296 ALNFEQTKVTLHCETQEDSLRTLYRFVHGVPLRHKSVMRCGASISFSLTT--ENSGN 352
Db 297 GQIIEGNNVLLICSAQSGSTVTFWSHKEG-RVRSIGRKTQRLAEHLVLTVKESDAGR 355
QY 353 YYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPILY 412
Db 356 YYCAADNVHSPILSTWIRVTIRVPVSHVPLTFRAPRAHTVVGDLLELHCESLRGSPILY 415
QY 413 QFHEDDAALERRSANSAGGVAISFSLTAHSGNYCYTADNGFGPORSKAVSLSVTPVSH 472
Db 416 RFYHEDVTLGNSAPSGGGASPNLSLTAHSGNYSCTADNGLGAQSHGVSLRVTVPVSR 475
QY 473 PVLTLSSAEALTPEGAVTLHCEVQRGSPQILYQFVHEDMPLVSSSTPSPVGRVVSFSLT 532
Db 476 PVLTLRPAQAQVVGDLLELHCESLRGSPILYWFYHEDDTLGNISAHSGGGASPNLSLT 535
QY 533 EGHSGNYCYTADNGFGPORSVSLFVTG 561
Db 536 TEHSGNYSCEADNGLGAQSHKWTNLNTG 564

RESULT 13

ADL06557
ID ADL06557 standard; protein; 733 AA.
XX AC ADL06557;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Human tumour-associated antigenic target (TAT) polypeptide #56.
XX KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
XX KW cancer; cytostatic.
XX OS Homo sapiens.
XX XX
XX PN WO2004016225-A2.
XX PD 26-FEB-2004.
XX PF 19-AUG-2003; 2003WO-US025892.
XX PR 19-AUG-2002; 2002US-0404809P.
XX PR 21-AUG-2002; 2002US-0405645P.
XX PR 23-SEP-2002; 2002US-0413192P.
XX PR 15-OCT-2002; 2002US-0419008P.
XX PR 15-NOV-2002; 2002US-0426847P.
XX PR 02-JUL-2003; 2003US-0484959P.
XX PA (GETH) GENENTECH INC.
XX PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
XX PI Spencer SD, Wu TD, Zhang Z;
XX DR WPI: 2004-257144/24.
XX DR N-PSDB; ADL06478.

XX PS Claim 2; SEQ ID NO 137; 319pp; English.
XX CC The present invention relates to the isolation of human tumour-associated
XX CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
XX CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
XX CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
XX CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
XX CC produced in bacteria or in CHO cells and induces death of a cell to which
XX CC it binds. The antibody is useful for preparing a composition for
XX CC diagnosing or treating tumours and cancer. The present sequence
XX CC represents a human TAT polypeptide of the invention.

Seq Sequence 733 AA;
Query Match 38.1%; Score 1191; DB 8; Length 733;
Best Local Similarity 45.3%; Pred. No. 2.3e-78;
Matches 258; Conservative 77; Mismatches 220; Indels 14; Gaps 7;
QY 1 MLLWVLLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVLTCKGRFFSPQ-KTKWYH 59
Db 1 MLLWVLLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVLTCKGRFFSPQ-KTKWYH 60
QY 60 RVLGKEILRETFPDNILEVQESGEVRCOAQSGPLSPVHLDFFSSASLILQAPLSVFEQDSV 119
Db 61 ---DEKLKIKHD--IQITEFGNQCKTRGSSLDADAVHVEFDPWLLILQALHPVFEQDNV 115
QY 120 VILRCRAKAEVTLNNTIYKNDVNLAPLNKRTDFHPLACLKNGAYRCTGYKESC---CPV 176
Db 116 LLRCQCKDNKNTQKVVYKDGKQLPNSYNLEKITVNSVRDNSKYHCTAYRKFYILDIEV 175
QY 177 SNTVKIQVQBPPTPVLRASSFOPISGNPVTLTCETOLSLERSDVPRLRFFRDDDTLG 236
Db 176 TSKPLNIQVELFLHPVLRASSTPIEGSPMTLTCETQLSPQRPDVQLOFLFRDSQTLG 235
QY 237 LGWSLSPNPQITAMWSKDSGFYWCATMPHSVSDSPRSWIQV-IPASHPVLTLSPEK 295
Db 236 LGWSRSPRLQIPAMWTEDSGSYKCEVETVTHSIKXSLRSQIRVQRPVSNVNLIRPTG 295
QY 296 ALNFEQTKVTLHCETQEDSLRTLYRFVHGVPLRHKSVMRCGASISFSLTT--ENSGN 352
Db 296 GQIIEGNNVLLICSAQSGSTVTFWSHKEG-RVRSIGRKTQRLAEHLVLTVKESDAGR 354
QY 353 YYCTADNGLGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPILY 412
Db 355 YYCAADNVHSPILSTWIRVTIRVPVSHVPLTFRAPRAHTVVGDLLELHCESLRGSPILY 414
QY 413 QFHEDDAALERRSANSAGGVAISFSLTAHSGNYCYTADNGFGPORSKAVSLSVTPVSH 472
Db 415 RFYHEDVTLGNSAPSGGGASPNLSLTAHSGNYSCTADNGLGAQSHGVSLRVTVPVSR 474
QY 473 PVLTLSSAEALTPEGAVTLHCEVQRGSPQILYQFVHEDMPLVSSSTPSPVGRVVSFSLT 532
Db 476 PVLTLRPAQAQVVGDLLELHCESLRGSPILYWFYHEDDTLGNISAHSGGGASPNLSLT 534
QY 533 EGHSGNYCYTADNGFGPORSVSLFVTG 561
Db 535 TEHSGNYSCEADNGLGAQSHKWTNLNTG 563

RESULT 14

ABB84668
ID ABB84668 standard; protein; 727 AA.
XX AC ABB84668;
XX XX
XX 11-FEB-2003 (first entry)
XX DE Human SECP-20 protein from clone 8039739CD1 SEQ ID 20.
XX XX

XX KW Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic;
XX KW hepatotropic; cytostatic; anti-HIV; antiallergic; antiasthmatic; cancer;
XX KW antianemic; antidiabetic; antiinflammatory; neuroprotective; antiulcer;
XX KW antithrombotic; antitubercular; cardiac; hypotensive; gonadal dysgenesis;
XX KW vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis;
XX KW antiparkinsonian; ophthalmological; cell proliferative disorder;
XX KW arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris;
XX KW autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy;
XX KW ulcerative colitis; cardiovascular disorder; myocardial infarction;
XX KW Raynaud's disease; myocardiitis; neurological disorder; cataract;
XX KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
XX KW developmental disorder; Duchenne muscular dystrophy; antipsoriatic;
XX KW Becker muscular dystrophy; Cushing's syndrome.

XX Homo sapiens.

XX OS

PN WO200279441-A2.
 XX 10-OCT-2002.
 XX 29-MAR-2002; 2002WO-US009820.
 XX 30-MAR-2001; 2001US-0280527P.
 PR 06-APR-2001; 2001US-0282112P.
 PR 09-APR-2001; 2001US-0282702P.
 PR 13-APR-2001; 2001US-0283855P.
 PR 19-OCT-2001; 2001US-0343718P.
 PR 07-DEC-2001; 2001US-0339236P.
 PR 13-FEB-2002; 2002US-0357002P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Baughn MR, Burford N, Ding L, Duggan BM, Elliott VS, Forsythe J;
 PI Gandhi AR, Gietzen KJ, Griffin JA, He A, Honchell CD, Ison CH;
 PI Lal PG, Lee EA, Lee S, Lu DAM, Mason PM, Sanjanwala MM;
 PI Swarnakar A, Rankumar J, Tang YT, Thangavelu K, Tran UK, Wallia NK;
 PI Warren BA, Yao MG, Xu Y, Yue H;
 XX WPI; 2003-058429/05.
 DR N-ESDB; ABS57564.
 XX Novel human secreted protein useful for treating, preventing or
 PT diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus,
 PT anemia, epilepsy, cataract, Alzheimer's disease.
 XX Claim 75; Page 165-166; 188pp; English.
 XX This invention describes novel secreted proteins (SECP) which have
 CC anti-arteriosclerotic, anti-atherosclerotic, hepatotropic, cytostatic, anti
 CC -HIV, anti-allergic, anti-asthmatic, anti-anemic, antidiabetic,
 CC anti-inflammatory, neuroprotective, anti-ulcer, antipsoriatic, vasotropic,
 CC antirheumatic, antiarthritic, cardiac, hypotensive, anticonvulsant,
 CC nootropic, immunosuppressive, antiparkinsonian and ophthalmological
 CC activity. The polynucleotides and polypeptides of the invention can be
 CC used for diagnosing, treating or preventing cell proliferative disorder
 CC e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, cancer,
 CC autoimmune/inflammatory disorders e.g. acquired immunodeficiency syndrome
 CC (AIDS), allergies, asthma, anaemia, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, ulcerative colitis, psoriasis, rheumatoid arthritis,
 CC etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris,
 CC hypertension, Raynaud's disease, myocarditis, pericarditis, etc;
 CC neurological disorders e.g. epilepsy, Huntington's disease, Parkinson's
 CC disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and
 CC developmental disorders e.g. Duchenne and Becker muscular dystrophy,
 CC cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of
 CC the invention can also be used for drug screening, proteome analysis,
 CC microarrays creating knock-in humanised animals or transgenic animals to
 CC model human diseases, in somatic or germline gene therapy, to generate a
 CC transcript image of a tissue or cell type, for detecting differences in
 CC the chromosomal location due to translocation, inversion, etc., among
 CC normal, carrier or affected individuals, and as hybridization probes for
 CC mapping naturally occurring genomic sequences. ABS84649-ABS84673
 CC represent secreted proteins encoded by the cDNA's shown in ABS57545-
 CC ABS57569, described in the disclosure of the invention
 XX Sequence 727 AA;
 SQ
 Query Match 37, 68; Score 1176; DB 6; Length 727;
 Best Local Similarity 45.28; Pred No. 2.9e-77;
 Matches 257; Conservative 76; Mismatches 216; Indels 20; Gaps 8;
 Qy 1 MLLWVLLVAPVSGQFARTPRIFIQPPTVFGQERVTLCKGRFYSPO-KTKWYH 59
 Db 1 MLLWVLLVAPVSGQFARTPRIFIQPPTVFGQERVTLCKGRFYSPO-KTKWYH 59
 Qy 60 RYLCKETLRTPPNILEVQSGEVRCAQSGPSSPVHLDFFSSASLILQAPLSVREGDSV 119
 Db 54 ---DEKLKIKHDKI-QITSPGNVQCKTRGSUSDAVHVEFSPDWLLIQALHPVFEQDNV 109

QY 120 VLRCEAKAEVTLNNTIYKNDVLAFLNKRTPDHPHACLKDNQAYRCTGYKESC---CPV 176
 DB 110 ILRCQKDNKNTKHKYVYKQKQLPNSYNLEKITVNSVSRDYSKTHCTAKRKFIILIEV 169
 QY 177 SSNTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPFRFRFFDDQTLG 236
 DB 170 TSKPLNIQVQLFLHPLVLRASSSTPIEGSPMTLCTQLSPQRPDVQLQFSLFRDSQTLG 229
 QY 237 LQWSLSPNFQITAMWSDGPFYCKAATMPHSVSDSPRSWIQVQ-IPASHPVLTLSPEK 295
 DB 230 LQWSRSPRLQIPAMWTEDSGSYCEVETVTHSIKRLSRQIRVQRFVSNVNLIEIRPTG 289
 QY 296 ALNPEGTKVTLHCETOEDSLTLYRFYHEGVPLRHKSVRCERGASISFSJTT---ENSGN 352
 DB 290 QQLIEGENWVLCVAGQSGTFTSMHKEG-RVSLGRKTOESLLAEHLVLTVKESDAGR 348
 QY 353 YYCTADNGLGAKPKAVSLSVTVVSHPVLMNLSPEDLIFEGAKVTLHCEAQRGSLPILY 412
 DB 349 YYCAADNVHSPILSTWIRTVRIPVSHPVLTFRAPRAHTVVGDLELHCESLRGSPPILY 408
 QY 413 QPHHEDAALERRSANSAGGVAISFSLTAHSGNYCTADNGFGFQSRKAVSLSTIVPVSH 472
 DB 409 RPYHEDVTLGNSSAPSGGGASFNLSLTAHSGNYCTADNGLGAQHSHGVSLRTVTVFSR 468
 QY 473 PVLTLSSAEALTFFEGATVTLHCEVQVQSPQILYQFYHEDMPLVSSSTPFSVGRVSFSLT 532
 DB 469 PVLTLRAPGAQAVVGDLELHCESLRGSFPILYWFYHEDDTLGNISAHSGGGASFNLSLT 528
 QY 533 EGHSGNYCTADNGFGFQSRSEVSLFVTG 561
 DB 529 TEHSGNVSCEADNGLGAQHSHGVSLRTVTVFSR 557
 RESULT 15
 ADF74336
 ID ADF74336 standard; protein; 554 AA.
 AC ADF74336;
 DT 26-FEB-2004 (first entry)
 DE Extracellular domain of the human FcRH3 protein (SeqID 24).
 KW Fc receptor homologue; FcRH; human; chromosome 1q21-23;
 KW type I transmembrane receptor; immunoglobulin; cellular immunity;
 KW haematopoietic cell lineage; inflammatory; autoimmune disease;
 KW humoral immune response; antiinflammatory; immunosuppressive.
 OS Homo sapiens.
 XX WO2003089624-A2.
 PD 30-OCT-2003.
 PF 25-MAR-2003; 2003WO-US009600.
 PR 25-MAR-2002; 2002US-0367667P.
 PA (UABR-) UAB RES FOUND.
 PI Davis RS, Cooper MD;
 DR WPI; 2003-854118/79.
 PT New isolated Fc receptor homologue (FcRH) comprising a cytoplasmic,
 PT transmembrane and an extracellular region, useful for the diagnosis
 PT and/or treatment of hematopoietic cell lineage, inflammatory and
 PT autoimmune diseases.
 PS Claim 30; SEQ ID NO 24; 135pp; English.
 CC This invention relates to novel members of the Fc receptor homologue
 CC (FcRH) subfamily mapped to human chromosome 1q21-23, as well as fragments

Search completed: November 30, 2004, 11:46:59
Job time : 157 secs

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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:39:56 ; Search time 39 Seconds

(without alignments)
1006.673 Million cell updates/sec

Title: US-09-724-254A-3

Perfect score: 3124

Sequence: 1 MLWVILLVLPVSGQFART.....AEPSLTHSPKFLFALSSFLP 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

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5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	12.4	261	US-09-245-764-7	Sequence 7, Appli
2	305.5	9.8	254	US-08-667-939A-3	Sequence 3, Appli
3	305.5	9.8	254	US-08-433-123-3	Sequence 3, Appli
4	304.5	9.7	254	US-08-667-939A-2	Sequence 2, Appli
5	304.5	9.7	254	US-08-433-123-2	Sequence 2, Appli
6	293	9.4	233	US-08-667-939A-6	Sequence 6, Appli
7	293	9.4	233	US-08-433-123-6	Sequence 6, Appli
8	292.5	9.4	254	US-08-667-939A-9	Sequence 9, Appli
9	292.5	9.4	254	US-08-433-123-9	Sequence 9, Appli
10	292	9.3	233	US-08-667-939A-5	Sequence 5, Appli
11	292	9.3	233	US-08-667-939A-8	Sequence 8, Appli
12	292	9.3	233	US-08-433-123-5	Sequence 5, Appli
13	292	9.3	233	US-08-433-123-8	Sequence 8, Appli
14	288.5	9.2	254	US-08-667-939A-4	Sequence 4, Appli
15	288.5	9.2	254	US-08-433-123-4	Sequence 4, Appli
16	286	9.2	233	US-08-667-939A-7	Sequence 7, Appli
17	286	9.2	233	US-08-433-123-7	Sequence 7, Appli
18	285.5	9.1	254	US-08-667-939A-1	Sequence 1, Appli
19	285.5	9.1	254	US-08-433-123-1	Sequence 1, Appli
20	275	8.8	197	US-08-788-954-2	Sequence 2, Appli
21	275	8.8	203	US-08-667-939A-20	Sequence 20, Appli
22	275	8.8	203	US-08-433-123-20	Sequence 20, Appli
23	274	8.8	174	US-09-245-764-8	Sequence 8, Appli
24	271	8.7	215	US-08-667-939A-18	Sequence 18, Appli
25	271	8.7	215	US-08-433-123-18	Sequence 18, Appli
26	269.5	8.6	199	US-08-768-964-12	Sequence 12, Appli
27	269.5	8.6	199	US-09-005-299-12	Sequence 12, Appli

28	269.5	8.6	199	3	US-09-515-431-12	Sequence 12, Appli
29	269.5	8.6	263	2	US-08-768-964-2	Sequence 2, Appli
30	269.5	8.6	263	3	US-09-005-299-2	Sequence 2, Appli
31	269.5	8.6	263	3	US-09-515-431-2	Sequence 2, Appli
32	267	8.5	197	2	US-08-756-387B-11	Sequence 11, Appli
33	267	8.5	197	3	US-09-285-873-11	Sequence 11, Appli
34	267	8.5	197	4	US-09-944-277A-11	Sequence 11, Appli
35	267	8.5	257	1	US-07-869-933-11	Sequence 11, Appli
36	267	8.5	257	2	US-08-756-387B-2	Sequence 2, Appli
37	267	8.5	257	3	US-09-103-663-11	Sequence 11, Appli
38	267	8.5	257	3	US-09-285-873-2	Sequence 2, Appli
39	267	8.5	257	4	US-08-897-956A-1	Sequence 1, Appli
40	267	8.5	257	4	US-09-944-277A-2	Sequence 2, Appli
41	267	8.5	978	4	US-08-897-956A-3	Sequence 3, Appli
42	266	8.5	307	2	US-08-332-562A-83	Sequence 83, Appli
43	265	8.5	193	2	US-08-765-536-1	Sequence 1, Appli
44	265	8.5	193	5	PCT-US95-08401-1	Sequence 1, Appli
45	257	8.2	261	2	US-08-332-562A-133	Sequence 133, App

ALIGNMENTS

RESULT 1

US-09-245-764-7
; Sequence 7, Application US/09245764
; Patent No. 6675105
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/09/245,764
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/099,994
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: 60/073,972
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-764-7

Query Match 12.4%; Score 386; DB 4; Length 261;
Best Local Similarity 35.7%; Pred. No. 6.2e-27;
Matches 95; Conservative 40; Mismatches 121; Indels 10; Gaps 6;

Qy	20	TPRPIIFLOPPWTTVFGGERVTLTCKGFRFSPQKTKWYHRLKELRTPD---NILE	76
Db	1	TTKAVITLQPPWVSFQEEVTILHCEVLPGLSSSTQWFVN--GTATQSTPSYRITSAS	58
Qy	77	VQSGEYRCQAQSPGLSSPVHLDFFSASLILOAPLSVF-EGDSVULRCRAKAEVTLNNTI	135
Db	59	VNDSGEYRCQGLSGRSDPTQLHHRGWLIIQVSSRVFTEGEPLALRCHAWKDKLYNVNL	118
Qy	136	YKNDNVLAFLNKETDHFHACIKDNGAYRCTGYKSCCPVSSNTVKIQVQEPFTRPVL	195
Db	119	YRNGKFKPFHWNSTLTILKTNISHNGTHCSMGKH--RYTSAGISVTVKELFPAPVLN	176
Qy	196	ASSFQIP-IGSNPVTLTCTETQLSLERSDVLPRFFRDOTLGLGWSLSNPNQITAMWSKD	254
Db	177	ASVTSPLLEGNLVTLSCTELKQRPGLQYFSGYMGSKTL-RCRNTSSEYQILTARRED	235
Qy	255	SGFWCKAATMPHSVSDSPRSNIQV 280	

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Db      236 SGLYWCBAATEDGNVLRSPLELQV 261

RESULT 2
US-08-667-939A-3
; Sequence 3, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-3

Query Match          9.8%; Score 305.5; DB 2; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.3e-19;
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

QY      1 MLLWVILLVAPVSGQPARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPQ--KTKWY 58
Db      4 LLLPTALLLVASAGMTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY      59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db      62 HK-----ENLISSQASSYFIDAATVDSGSEYRCQTNLTSLSDPVQLEVQVGWLL 110
QY      107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKETDFHPEACIKONGAY 164
Db      111 LQAPRWFKBEDPTHLRCHSWKNTALHKVTYLONGKDKRYFHNSDFHIPKATLKDSGSY 170
QY      165 RCTGYKESCCPVSSNTVKIQVEBFTPRVLRASSFQISGNPVTLTCTQLSLERSDVPL 224
Db      171 FCRGLVGS-KNVSSETNIIITQGLA--VSTISFFP-PGYQVSF-CLNVVLLFAVDT-- 223
QY      225 RFRFRDDQTLGLGWSLSPNFQITAMMSKDSGFYCK 261
Db      224 -----GLYFSVKTNIIRSTRDKDKHKFKWK 249

RESULT 3
US-08-433-123-3
; Sequence 3, Application US/08433123

```

```

; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-3

Query Match          9.8%; Score 305.5; DB 4; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.3e-19;
Matches 91; Conservative 37; Mismatches 102; Indels 47; Gaps 11;

QY      1 MLLWVILLVAPVSGQPARTPRPIIFLOPPWTVTFQGERVTLTKGFRFYSPQ--KTKWY 58
Db      4 LLLPTALLLVASAGMTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY      59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQGSPLSSPVHLDFSSASLI 106
Db      62 HK-----ENLISSQASSYFIDAATVDSGSEYRCQTNLTSLSDPVQLEVQVGWLL 110
QY      107 LQAPLSVP-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKETDFHPEACIKONGAY 164
Db      111 LQAPRWFKBEDPTHLRCHSWKNTALHKVTYLONGKDKRYFHNSDFHIPKATLKDSGSY 170
QY      165 RCTGYKESCCPVSSNTVKIQVEBFTPRVLRASSFQISGNPVTLTCTQLSLERSDVPL 224
Db      171 FCRGLVGS-KNVSSETNIIITQGLA--VSTISFFP-PGYQVSF-CLNVVLLFAVDT-- 223
QY      225 RFRFRDDQTLGLGWSLSPNFQITAMMSKDSGFYCK 261
Db      224 -----GLYFSVKTNIIRSTRDKDKHKFKWK 249

RESULT 4
US-08-667-939A-2
; Sequence 2, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK

```

```
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEO=2A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-2

Query Match          9.7%; Score 304.5; DB 2; Length 254;
Best Local Similarity 32.9%; Pred. No. 1.6e-19;
Matches 91; Conservative 38; Mismatches 101; Indels 47; Gaps 11;

QY 1 MLLWVLLVLPVSGQPARTPRPIIFLOPPMTTTFQGERVLTICKGFRFYSPQ--KTKWY 58
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 4 LLLPTALLLVAGNRTEDLPKAVVLEPQWYVLEKDSVTLKCOG--AYSPEDNSTQWF 61
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 59 HRYLGKEILRETPDNILE-----VOESGEYRCQAQGSPLSSPVHLDFSSASLI 106
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 62 HK-----ENLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVQVGWLL 110
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 107 LOAPLSVFP-EGDSVVLRCAKAEVLTNNIY-KNDNVLAFLNKRDTDFHIFHACLKNGAY 164
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 111 LOAPRWVFEEDPIHLRCHSWKNTALHKVTVLQNGKDRKYFHNSDFHIFKATLKDSGSY 170
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 165 RCTGYKESCCPVSSNTVKIQVQEPTRPVLRASSFPQISGNPVTLTCTQLSLERSDVPL 224
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 171 FCKGLVGS-KNVSSTVNITIIQGLA--VSTNSSFFP-PGYQVSF-CLVMVLLFAVDT-- 223
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 225 RFRFRDDOTLGLGWSLSNFOITAMWSKDSGFYWK 261
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 224 -----GLYFSVKTNIRSTRDWKDKHFKWRK 249
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 5
US-08-433-123-2
; Sequence 2, Application US/08433123
; Patent No. 644789
; GENERAL INFORMATION:
; APPLICANT: LEO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
```

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-667-939A-6

Query Match 9.4%; Score 293; DB 2; Length 233;
Best Local Similarity 34.7%; Pred. No. 1.6e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQMF 61
QY 59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQSPVHLDPFSSASLI 106
Db 62 HN-----ENLISSQAASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110
QY 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKETDFHPIHACLKNGAY 164
Db 111 LQAPRWVFEEDPIHLRCHSWKNTALHKVTYVQNGKDRKYFHNSDFHPIKATLKDSGSY 170
QY 165 RCTGYKSCCPVSNVTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPL 224
Db 171 FCRLGVSG-KNVSETVNIITQGLA--VSTISSFSP-PGVQVSF-CLVNVLLFAVDVDTGL 225
QY 225 RF 226
Db 226 YF 227

RESULT 7
US-08-433-123-6
; Sequence 6, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-6

Query Match 9.4%; Score 293; DB 4; Length 233;
Best Local Similarity 34.7%; Pred. No. 1.6e-18;
Matches 84; Conservative 32; Mismatches 92; Indels 34; Gaps 10;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVLSAGMRTEDLPKAVVLEPQWRYVLEKDSVTLKCG--AYSPEDNSTQMF 61
QY 59 HRYLGKEILRETPDNILE-----VQESGEYRCQAQSPVHLDPFSSASLI 106
Db 62 HN-----ENLISSQAASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEHVHVGWLL 110
QY 107 LQAPLSVF-EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKETDFHPIHACLKNGAY 164
Db 111 LQAPRWVFEEDPIHLRCHSWKNTALHKVTYVQNGKDRKYFHNSDFHPIKATLKDSGSY 170
QY 165 RCTGYKSCCPVSNVTVKIQVQEPFTRPVLRASSFQISGNPVTLTCTQLSLERSDVPL 224
Db 171 FCRLGVSG-KNVSETVNIITQGLA--VSTISSFSP-PGVQVSF-CLVNVLLFAVDVDTGL 225
QY 225 RF 226
Db 226 YF 227

RESULT 8
US-08-667-939A-9
; Sequence 9, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids

; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-667-939A-9
 Query Match
 Best Local Similarity 9.4%; Score 292.5; DB 2; Length 254;
 Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;
 QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFYSPQ--KTKWY 58
 Db 4 LLLPTALLLVLSAGMRTEDLPKAVFLEPQYRVLKDSVTLKCG--AYSPEDNSTQWF 61
 QY 59 HRYLGEILRETPDNIL----EVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVF 114
 Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118
 QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRDTDEHPHACKLKDNGAYRCTGYKES 172
 Db 119 KEEDPIHLRCHSWKNTALHKVTYLQNGKGRKYFHNSDFYIPKATLKDSGSGYFCRGLFGS 178
 QY 173 CCPVSSNTVKIQVQEPFTRPVLRASFPQISGNPVTLTCETQLSLERSDVLPRFRFRDD 232
 Db 179 -KNWSSEVNTITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223
 QY 233 QTLGLGWSLSNFOITAMWSKDSGFYCK 261
 Db 224 ---GLYFSVKTNIIRSTRDWKDKHFKWRK 249

RESULT 9
 US-08-433-123-9
 ; Sequence 9, Application US/08433123
 ; Patent No. 644789
 ; GENERAL INFORMATION:
 ; APPLICANT: LUO, Shun
 ; TITLE OF INVENTION: CD16-II VARIANTS
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/433,123
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: LUO-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 254 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-433-123-9
 Query Match
 Best Local Similarity 9.4%; Score 292.5; DB 4; Length 254;
 Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;

Best Local Similarity 33.1%; Pred. No. 2e-18;
 Matches 89; Conservative 38; Mismatches 111; Indels 31; Gaps 11;
 QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFYSPQ--KTKWY 58
 Db 4 LLLPTALLLVLSAGMRTEDLPKAVFLEPQYRVLKDSVTLKCG--AYSPEDNSTQWF 61
 QY 59 HRYLGEILRETPDNIL----EVOESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVF 114
 Db 62 H---NESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLOAPRWVF 118
 QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRDTDEHPHACKLKDNGAYRCTGYKES 172
 Db 119 KEEDPIHLRCHSWKNTALHKVTYLQNGKGRKYFHNSDFYIPKATLKDSGSGYFCRGLFGS 178
 QY 173 CCPVSSNTVKIQVQEPFTRPVLRASFPQISGNPVTLTCETQLSLERSDVLPRFRFRDD 232
 Db 179 -KNWSSEVNTITQGLA--VSTISSFPF-PGYQVSF-CLVMVLLFAVDT----- 223
 QY 233 QTLGLGWSLSNFOITAMWSKDSGFYCK 261
 Db 224 ---GLYFSVKTNIIRSTRDWKDKHFKWRK 249

RESULT 10
 US-08-667-939A-5
 ; Sequence 5, Application US/08667939A
 ; Patent No. 598166
 ; GENERAL INFORMATION:
 ; APPLICANT: LUO, Shun
 ; TITLE OF INVENTION: CD16-II VARIANTS
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/667,939A
 ; FILING DATE: 24-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/433,123
 ; FILING DATE: 03-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: LUO-2A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-667-939A-5
 Query Match
 Best Local Similarity 35.5%; Pred. No. 1.9e-18;
 Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;
 QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKCKGRFYSPQ--KTKWY 58
 Db 4 LLLPTALLLVLSAGMRTEDLPKAVFLEPQYRVLKDSVTLKCG--AYSPEDNSTQWF 61

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QY 59 HRYLGKILRETPDNIL-----EVCESGEYRCQAGSPSSPVHLDPSASLILOAPLSVF 114
DB 62 H---NESLISSQASSYFIDATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRTRDFHHPHACLKNDGAYRCTGYKES 172
DB 119 KEEDPIHLRCHSWKNTALHKVTYVLQNGKDRKYFHNSDFHHPKATLKDSGYSYFCRGLVGS 178
QY 173 CCPVSSNTVKIQVEPTRPVLRASSFPQISGNPVTLTCTQSLERSDVPPLRF 226
DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 11
US-08-667-939A-8
; Sequence 8, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LEO-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-667-939A-8

Query Match 9.3%; Score 292; DB 2; Length 233;
Best Local Similarity 35.5%; Pred. No. 1.9e-18;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
DB 4 LLLPTALLLVSAAGMRTEDLPKAVFLEPQWYVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGKILRETPDNIL-----EVCESGEYRCQAGSPSSPVHLDPSASLILOAPLSVF 114
DB 62 H---NESLISSQASSYFIDATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRTRDFHHPHACLKNDGAYRCTGYKES 172
DB 119 KEEDPIHLRCHSWKNTALHKVTYVLQNGKDRKYFHNSDFHHPKATLKDSGYSYFCRGLVGS 178
QY 173 CCPVSSNTVKIQVEPTRPVLRASSFPQISGNPVTLTCTQSLERSDVPPLRF 226
DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 13
US-08-433-123-8
; Sequence 8, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS

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DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 12
US-08-433-123-5
; Sequence 5, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,123
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LEO-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEPHAX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-5

Query Match 9.3%; Score 292; DB 4; Length 233;
Best Local Similarity 35.5%; Pred. No. 1.9e-18;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
DB 4 LLLPTALLLVSAAGMRTEDLPKAVFLEPQWYVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGKILRETPDNIL-----EVCESGEYRCQAGSPSSPVHLDPSASLILOAPLSVF 114
DB 62 H---NESLISSQASSYFIDATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGSVVLRCAKAEVTLNNTIY-KNDNVLAFLNKRTRDFHHPHACLKNDGAYRCTGYKES 172
DB 119 KEEDPIHLRCHSWKNTALHKVTYVLQNGKDRKYFHNSDFHHPKATLKDSGYSYFCRGLVGS 178
QY 173 CCPVSSNTVKIQVEPTRPVLRASSFPQISGNPVTLTCTQSLERSDVPPLRF 226
DB 179 -KNVSSETVNTITQGLA--VSTISSFSF-PGYQVSF-CLVMVLLFAVDITGLYF 227

RESULT 13
US-08-433-123-8
; Sequence 8, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-667-939A-4

Query Match 9.2%; Score 288.5; DB 2; Length 254;
Best Local Similarity 33.1%; Pred. No. 4.6e-18;
Matches 89; Conservative 37; Mismatches 112; Indels 31; Gaps 11;

QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
DB 4 LLLPTALLLLVNSAGMTEDELPKAVVLEPQWVRLKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGEILRETPDNIL-----EVQSGEYRCAQCSPLSSPVHLDFFSSASLILQAPLSVF 114
DB 62 H--NESLISSQASSYFIDAATVDDSGEYRCQTNLTSLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPHACIKDNGAYRCTGYKES 172
DB 119 KEEDPHLCHSKWNTALHKVTYLONGKGRKYSHNSDFYIPKATLKDSGSGYFCRGLVGS 178
QY 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPISGNPNVTLTCTQLSLERSDVPLRFRRDD 232
DB 179 -KNVSETVNIITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDVT----- 223
QY 233 QTLGLWSLSPNQITAMWSKDSGFYCK 261
DB 224 ---GLYFSVKTNIRSPTRDNKDKHFKWRK 249

RESULT 15
US-08-433-123-4
Sequence 4, Application US/08433123
Patent No. 644789
GENERAL INFORMATION:
APPLICANT: LUO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LWO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-123-8

Query Match 9.3%; Score 292; DB 4; Length 233;
Best Local Similarity 35.5%; Pred. No. 1.9e-18;
Matches 83; Conservative 34; Mismatches 99; Indels 18; Gaps 10;

QY 1 MLLWVLLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTKGFRFYSPQ--KTKWY 58
DB 4 LLLPTALLLLVNSAGMTEDELPKAVVLEPQWVRLKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGEILRETPDNIL-----EVQSGEYRCAQCSPLSSPVHLDFFSSASLILQAPLSVF 114
DB 62 H--NESLISSQASSYFIDAATVDDSGEYRCQTNLTSLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGDSVVLRCRAKAEVTLNNTIY-KNDNVLAFLNKRTPHACIKDNGAYRCTGYKES 172
DB 119 KEEDPHLCHSKWNTALHKVTYLONGKDRKTFHNSDFHPIKATLKDSGSGYFCRGLVGS 178
QY 173 CCPVSSNTVKIQVQEPFTRPVLRASSFPISGNPNVTLTCTQLSLERSDVPLRF 226
DB 179 -KNVSETVNIITQGLA--VSTISSFSP-PGYQVSF-CLVMVLLFAVDVTGLYF 227

RESULT 14
US-08-667-939A-4
Sequence 4, Application US/08667939A
Patent No. 598166
GENERAL INFORMATION:
APPLICANT: LUO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LEO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-123-4

Query Match          9.2%; Score 288.5; DB 4; Length 254;
Best Local Similarity 33.1%; Pred. No. 4.6e-18;
Matches 89; Conservative 37; Mismatches 112; Indels 31; Gaps 11;

QY 1 MLLWVILLVLPVSGQPARTPRPIIFLQPPWTTVFQGERVTLCKGFRFYSPQ--KTKWY 58
Db 4 LLLPTALLLVSAQMRTEDLPKAVVELEPQYRVLEKDSVTLKCG--AYSPEDNSTQWF 61
QY 59 HRYLGKEILRETPDNIL-----EVOESGEYRCQACQSPVHLDFFSSASLIILQAPLSVF 114
Db 62 H--NESLISSQASSYFIDATVDSDGEYRCQTNLSTLSDPVQLEVHIGWLLQAPRWVF 118
QY 115 -EGDSVILRCRAKAEVILNNTIY-KNDNVLAFLNKRTPDFHPRACLKNGAYRCTGYKES 172
Db 119 KEEDPIHLRCHSWKNTALHKVTLQNGKGRKYSHHNSDFYIPKATLKSGSYFCRGLFGS 178
QY 173 CCPVSSNTVKIQOEPFTRPVLRRASSFQPISGNPNVTLTCETQLSLERSDVLPRFRFRDD 232
Db 179 -KNYSSETVNTITQGLA--VSTISSFPF-PGYQVSP-CLVMVLLFAVDT----- 223
QY 233 QTLGLGWSLSPNFOITAMWSKDSGFYWK 261
Db 224 ---GLYFSVKTNIRSPTRDWDKDKFKWK 249

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 30, 2004, 11:44:31 ; Search time 144 Seconds

(without alignments)
1458.190 Million cell updates/sec

Title: US-09-724-254A-3

Perfect score: 3124

Sequence:

Scoring table: BLOSUM62

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Searched: 1575965 seqs, 354694765 residues

Total number of hits satisfying chosen parameters: 1575965

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3111	99.6	592	14	US-10-040-862-10461
2	3111	99.6	592	15	US-10-057-475B-10461
3	3111	99.6	592	15	US-10-154-884B-10461
4	3111	99.6	592	15	US-10-403-847-8
5	3111	99.6	592	16	US-10-764-324-10461
6	2950	94.4	759	14	US-10-040-862-10460
7	2950	94.4	759	15	US-10-057-475B-10460
8	2950	94.4	759	15	US-10-154-884B-10460
9	2950	94.4	759	15	US-10-403-847-7
10	2950	94.4	759	16	US-10-764-324-10460
11	2950	94.4	977	14	US-10-040-862-10462
12	2950	94.4	977	14	US-10-241-220-97
13	2950	94.4	977	15	US-10-057-475B-10462

Sequence 10462, A
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Sequence 10462, A
Sequence 97, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 94, Appli
Sequence 4774, Ap
Sequence 10463, A
Sequence 10463, A
Sequence 10463, A
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Sequence 2410, Ap
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Sequence 98, Appl
Sequence 10, Appl
Sequence 100, App
Sequence 11043, A
Sequence 10464, A
Sequence 10464, A
Sequence 11039, A
Sequence 10464, A
Sequence 458, App
Sequence 11052, A

US-10-154-884B-10462
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US-10-872-972-97
US-10-403-847-4
US-10-403-847-6
US-10-403-847-2
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US-10-040-862-10463
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US-10-764-324-10463
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US-10-408-765A-2410
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US-10-040-862-10464
US-10-057-475B-10464
US-10-154-884B-10464
US-10-154-884B-11039
US-10-764-324-10464
US-10-363-829-458
US-10-154-884B-11052

ALIGNMENTS

RESULT 1

US-10-040-862-10461
; Sequence 10461, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416

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; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10461

Query Match      99.6%; Score 3111; DB 14; Length 592;
Best Local Similarity 99.7%; Pred. No. 1.7e-232;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Qy 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLLIQAPLSVFEQDSVV 120
Db 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLLIQAPLSVFEQDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNRTDFPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNRTDFPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Qy 301 GTKVTLCETQEDSLRILYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
Db 301 GTKVTLCETQEDSLRILYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
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Db 421 LERSANSAGVAILSFSLTAEHSGNYCTADNGFGPQRSKAVSLITVPVSHVPLTLSSA 480
Qy 481 EALTFEAGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTECHSGNYY 540
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RESULT 2

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US-10-057-475B-10461
; Sequence 10461, Application US/10057475B
; Publication No. US2004002069A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
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; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10461
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Query Match      99.6%; Score 3111; DB 15; Length 592;
Best Local Similarity 99.7%; Pred. No. 1.7e-232;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVTLTCKGFRFYSPOKTKWYHR 60
Qy 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLLIQAPLSVFEQDSVV 120
Db 61 YLGEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDFSSASLLIQAPLSVFEQDSVV 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNRTDFPHACLKONGAYRCTGYKESCCPVSSNT 180
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNRTDFPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDQTLGLGWS 240
Db 181 VKIQVQEPFTRPVLRASSFQIPISGNPVTLTCTQLSLERSDVPRLRFRFRDDQTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Db 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVSDSPRSWIQVQIPASHPVLTLSPKALNFE 300
Qy 301 GTKVTLCETQEDSLRILYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
Db 301 GTKVTLCETQEDSLRILYRFYHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERSANSAGVAILSFSLTAEHSGNYCTADNGFGPQRSKAVSLITVPVSHVPLTLSSA 480
Db 421 LERSANSAGVAILSFSLTAEHSGNYCTADNGFGPQRSKAVSLITVPVSHVPLTLSSA 480
Qy 481 EALTFEAGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTECHSGNYY 540
Db 481 EALTFEAGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTECHSGNYY 540
```

	Query Match	99.6%; Score 3111; DB 15; Length 592;
	Best Local Similarity	99.7%; Pred. No. 1.7e-232;
	Matches 590; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy	1	MLLWVLLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGPRFFSPQKTKWYHR 60
Db	1	MLLWVLLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGPRFFSPQKTKWYHR 60
Qy	61	YLGKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDSSASLLIQAPLSVPEGDSV 120
Db	61	YLGKEILRETPDNILEVQESGEYRCQAQGSPLSPVHLDSSASLLIQAPLSVPEGDSV 120
Qy	121	LRCRAKAEVTLNNTIYKQNDVLAFLNKRTPHFPHACLKONGAYRCTGYKESCCPVSSNT 180
Db	121	LRCRAKAEVTLNNTIYKQNDVLAFLNKRTPHFPHACLKONGAYRCTGYKESCCPVSSNT 180
Qy	181	VKIQVQPEFTPRVLRASSFQPISGNPVTLTCEIQLSLERSDVPRLRFFRDRDQTLGLGWS 240
Db	181	VKIQVQPEFTPRVLRASSFQPISGNPVTLTCEIQLSLERSDVPRLRFFRDRDQTLGLGWS 240
Qy	241	LSPNFQITAMWXSQSGFYWCXAAATMPISVTSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Db	241	LSPNFQITAMWXSQSGFYWCXAAATMPISVTSDSPRSWIQVQIPASHPVLTLSPEKALNFE 300
Qy	301	GTKVTLTCEIQTEDSRLTYRFYHGVPLRHKSVRCERGASISFSLTITENSGNYICTADNG 360
Db	301	GTKVTLTCEIQTEDSRLTYRFYHGVPLRHKSVRCERGASISFSLTITENSGNYICTADNG 360
Qy	361	LGAKPSKAVSVTVTPVSPHVLNLSPPEDLIPEGAKVTLHCEAQKSGSLPILYQFHEDAA 420

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Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Db 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Qy 541 CTADNGFGPORSSEVSVLFTGKWCWLASKPPLAEFSLTHSFKNLFASSFLP 592
Db 541 CTADNGFGPORSSEVSVLFTGKWCWLASHPPLAEFSLTHSFKNLFASSFLP 592

RESULT 5
US-10-764-324-10461
; Sequence 10461, Application US/10764324
; Publication No. US2004017539A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10461
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10461

Query Match 99.6%; Score 3111; DB 16; Length 592;
Best Local Similarity 99.7%; Pred. No. 1.7e-232;
Matches 590; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLLWVILLVAPVSGQPARTPRIIFLOPPWTTVFGQERVTLTKGFRFYSQKTKWYHR 60
Db 1 MLLWVILLVAPVSGQPARTPRIIFLOPPWTTVFGQERVTLTKGFRFYSQKTKWYHR 60
Qy 61 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEQDSVY 120
Db 61 YLKGKILRETPDNILEVOESGEYRCQAQGSPLSSPVHLDFSSASLILOAPLSVFEQDSVY 120
Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHI PHACKLKDNGAYRCTGYKESCCPVSSNT 180
```

```
Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRDTFPHI PHACKLKDNGAYRCTGYKESCCPVSSNT 180
Qy 181 VKIQVEBPFTEPVLIRASSFOPISGNPVTLTCETOLSLERSDVLRRFRFRDDOTLGLGWS 240
Db 181 VKIQVEBPFTEPVLIRASSFOPISGNPVTLTCETOLSLERSDVLRRFRFRDDOTLGLGWS 240
Qy 241 LSPNFQITAMWSKDSGFWYCKAATMPHSVSDSPRSWIQVQIPASHVPLTISPEKALNFE 300
Db 241 LSPNFQITAMWSKDSGFWYCKAATMPHSVSDSPRSWIQVQIPASHVPLTISPEKALNFE 300
Qy 301 GTKVTLHCETOEDSLRTLRYFHYHGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360
Db 301 GTKVTLHCETOEDSLRTLRYFHYHGVPLRHKSVCRCGASISFSLTTENSGNYCTADNG 360
Qy 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Db 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
Qy 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Db 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPORSKAVSLSVTPVSHPVLTLSA 480
Qy 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Db 481 EALTFFEGATVTLHCEVORGSPQILYQFYHEDMPLVSSSTPSVGRVFSFSLTEGHSNGY 540
Qy 541 CTADNGFGPORSSEVSVLFTGKWCWLASKPPLAEFSLTHSFKNLFASSFLP 592
Db 541 CTADNGFGPORSSEVSVLFTGKWCWLASHPPLAEFSLTHSFKNLFASSFLP 592

RESULT 6
US-10-040-862-10460
; Sequence 10460, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
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; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10460

Query Match
Best Local Similarity 94.4%; Score 2950; DB 14; Length 759;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOQTKMYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOQTKMYHR 60
QY 61 YLCKEILRETPDNILLEVQESGYRCQAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120
DB 61 YLCKEILRETPDNILLEVQESGYRCQAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNLVAFLNKRTDPhiPHACLKNDGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNLVAFLNKRTDPhiPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPTPRVLRASSFQPISGNPVLTCTQSLERSDVPLRFRFRDDQTLGLWS 240
DB 181 VKIQVEPTPRVLRASSFQPISGNPVLTCTQSLERSDVPLRFRFRDDQTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYKCAATMPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYKCAATMPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVRCERGASISFSLTTTNSGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVRCERGASISFSLTTTNSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420
DB 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQSGPILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTPEGATVTLHCEVQSGPILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 572
DB 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 568
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RESULT 7

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US-10-057-475B-10460
; Sequence 10460, Application US/10057475B
; Publication No. US2004000268A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
```

```
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-10460
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Query Match 94.4%; Score 2950; DB 15; Length 759;

Best Local Similarity 98.4%; Pred. No. 7.1e-220;

Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

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QY 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOQTKMYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTVFQGERVLTCKGFRFYSPOQTKMYHR 60
QY 61 YLCKEILRETPDNILLEVQESGYRCQAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120
DB 61 YLCKEILRETPDNILLEVQESGYRCQAQGSPLSSPVHLDFSSASLILQAPLSVEGDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNLVAFLNKRTDPhiPHACLKNDGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNLVAFLNKRTDPhiPHACLKNDGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVEPTPRVLRASSFQPISGNPVLTCTQSLERSDVPLRFRFRDDQTLGLWS 240
DB 181 VKIQVEPTPRVLRASSFQPISGNPVLTCTQSLERSDVPLRFRFRDDQTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYKCAATMPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYKCAATMPHSVISDSPRSMTQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVRCERGASISFSLTTTNSGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYRHYEGVPLRHKSVRCERGASISFSLTTTNSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420
DB 361 LGAKPSKAVSLSVTVPVSHPVNLSSPEDLIPEGAKVTLHCEAQRGSPLILYQFHHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYCTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 480
QY 481 EALTPEGATVTLHCEVQSGPILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTPEGATVTLHCEVQSGPILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 572
DB 541 CTADNGFGQPSKAVSLSVTVPVSHPVLTLSA 568
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RESULT 8

US-10-154-884B-10460
; Sequence 10460, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-10460

Query Match 94.4%; Score 2950; DB 15; Length 759;
Best Local Similarity 98.4%; Pred. No. 7.1e-220;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
QY 61 YLGEILRETPDNTILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEGDSV 120
DB 61 YLGEILRETPDNTILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEGDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLWS 240
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVILSDSPRSWIOVQIPASHVPLTILSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVILSDSPRSWIOVQIPASHVPLTILSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
QY 360 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
DB 360 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420

RESULT 9

US-10-403-847-7
; Sequence 7, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICING VARIANTS OF A HUMAN
; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOLOGICAL FOLDS, BGS5G AND BGS5I
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patent version 3.2
; SEQ ID NO 7
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-7

Query Match 94.4%; Score 2950; DB 15; Length 759;
Best Local Similarity 98.4%; Pred. No. 7.1e-220;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
DB 1 MLLWVILLVLPVSGQFARTPRPIIFLQPPMTTVFQGERVTLCKGFRFYSPQKTKWYHR 60
QY 61 YLGEILRETPDNTILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEGDSV 120
DB 61 YLGEILRETPDNTILEVQESGEYRCQAQGSPLSPVHLDFSSASLILOAPLSVFEGDSV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLWS 240
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETQLSLERSDVPPLRFRFRDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVILSDSPRSWIOVQIPASHVPLTILSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVILSDSPRSWIOVQIPASHVPLTILSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLRYFYHEGVPLRHKSVRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTVPVSHVPLNLSPPEDLIFEGAKVTLHCEAQRGSLPILYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYCYCTADNGFGPORSKAVSLSVTVPVSHVPLTILSPEKALNFE 480

Db 421 LERRSANGGVAISFSLTAHSGNYCTADNGFGPQRKAVSLSLITVPVSHVLTLSA 480
QY 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSPFSLSLTEGHSNGNY 540
Db 481 EALTFFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSPFSLSLTEGHSNGNY 540
QY 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPL 572
Db 541 CTADNGFGPQRSEVSLFVTGKCVLASKPPL 572
RESULT 10
US-10-764-324-10460
; Sequence 10460, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10457
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10460

Query Match 94.4%; Score 2950; DB 16; Length 759;
Best Local Similarity 98.4%; Pred. No. 7,1e-220;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLWLWVLLVAPVSGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
Db 1 MLWLWVLLVAPVSGFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
QY 61 YLGKETLRETPDNILEVQSGEYRCQAQGSPLSSPVHLDFSSASLILQAPLSVFFGDSV 120
Db 61 YLGKETLRETPDNILEVQSGEYRCQAQGSPLSSPVHLDFSSASLILQAPLSVFFGDSV 120
QY 121 LACRAKAYVTLNNTIYKNDNVLAFLNKRTRDFHIFACLDKNGAYRCTGYKESCCFVSNT 180
Db 121 LACRAKAYVTLNNTIYKNDNVLAFLNKRTRDFHIFACLDKNGAYRCTGYKESCCFVSNT 180
QY 181 VKIQVQEPTRPVLRASSFQPISGNPVTLTCTQSLERSDVPLRFRFRDDQTLGLWS 240

RESULT 11
US-10-040-862-10462
; Sequence 10462, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10457
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10460
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10460

ORGANISM: Homo sapiens
US-10-040-862-10462

Query Match 94.4%; Score 2950; DB 14; Length 977;

Best Local Similarity 98.4%; Pred. No. 1e-219;

Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
QY 61 YLGEIILRETPDNTILEVQESGEYRCQAGSPVHLDFSSASLILOAPLSVFEQDSVV 120
DB 61 YLGEIILRETPDNTILEVQESGEYRCQAGSPVHLDFSSASLILOAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSLERSDVPLRFRFRDDQDTLGLWS 240
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSLERSDVPLRFRFRDDQDTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQGSLPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQGSLPLIYQFHEDAA 420
QY 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
DB 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
QY 481 EALFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQRSSEVVSFLVTGKCMWLASKPPL 572
DB 541 CTADNGFGPQRSSEVVSFLVTGKCMWLASKPPL 568

RESULT 12

US-10-241-220-97

Sequence 97, Application US/10241220

Publication No. US20030148408A1

GENERAL INFORMATION:

APPLICANT: Frantz, Gretchen

APPLICANT: Hillan, Kenneth J.

APPLICANT: Phillips, Heidi

APPLICANT: Polakis, Paul

APPLICANT: Spencer, Susan

APPLICANT: Williams, P. Mickey

APPLICANT: Wu, Thomas

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

FILE REFERENCE: P5010R1-US

CURRENT APPLICATION NUMBER: US/10/241,220

CURRENT FILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 97

LENGTH: 977

TYPE: PRT

ORGANISM: Homo Sapien

US-10-241-220-97

Query Match 94.4%; Score 2950; DB 14; Length 977;

Best Local Similarity 98.4%; Pred. No. 1e-219;

Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTKGFRFYSPOKTKWYHR 60
QY 61 YLGEIILRETPDNTILEVQESGEYRCQAGSPVHLDFSSASLILOAPLSVFEQDSVV 120
DB 61 YLGEIILRETPDNTILEVQESGEYRCQAGSPVHLDFSSASLILOAPLSVFEQDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTDPHIFACLDKNGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSLERSDVPLRFRFRDDQDTLGLWS 240
DB 181 VKIQVQEPFTRPVLRASSFPQISGNPVTLCETOLSLERSDVPLRFRFRDDQDTLGLWS 240
QY 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFOITAMWSKDSGFYWCKAATMPHSVSDSPRSWIOVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
DB 301 GTKVTLCETQEDSLRTLYRFYHEGVPLRHKSVCERGASISFSLTTENSGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQGSLPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSPEDLIFEGAKVTLHCEAQGSLPLIYQFHEDAA 420
QY 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
DB 421 LERSANSAGGVAISFSLTAHSGNYCTADNGFGPQRSKAVSLITVPVSHPVLTLSA 480
QY 481 EALFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALFEGATVTLHCEVQSGPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGPQRSSEVVSFLVTGKCMWLASKPPL 572
DB 541 CTADNGFGPQRSSEVVSFLVTGKCMWLASKPPL 568

RESULT 13

US-10-057-475B-10462

Sequence 10462, Application US/10057475B

Publication No. US2004002068A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Mannion, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Clapper, Jonathan David

APPLICANT: Wang, Aijun

APPLICANT: Ordonez, Nadia

APPLICANT: Carter, Lauren

APPLICANT: McNeill, Patricia Dianne

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-014402US

CURRENT APPLICATION NUMBER: US/10/057,475B

CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 10979
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10462
;; LENGTH: 977
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-057-475B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 1e-219;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYHR 60
QY 61 YLKGKILRETPDNILEVQESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120
DB 61 YLKGKILRETPDNILEVQESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVOEPFTRPVLASSQFISGNBPVTLTCTQLSLERSDVPRLFRFRDDQTLGLWS 240
DB 181 VKIQVOEPFTRPVLASSQFISGNBPVTLTCTQLSLERSDVPRLFRFRDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQKGSPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQKGSPLIYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
DB 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540
QY 541 CTADNGFGQPSGEVSVSLFVTGKCVLASKPPL 572
DB 541 CTADNGFGQPSGEVSVSLFVTGKCVLASKPPL 568

RESULT 14
US-10-154-884B-10462
; Sequence 10462, Application US/10154884B
; Publication No. US20040005561A
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane

;; APPLICANT: Retter, Marc W.
;; APPLICANT: Corixa Corporation
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
;; FILE REFERENCE: 014058-013521US
;; CURRENT APPLICATION NUMBER: US/10/154,884B
;; CURRENT FILING DATE: 2002-05-23
;; PRIOR APPLICATION NUMBER: US 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: US 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 11290
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10462
;; LENGTH: 977
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-154-884B-10462

Query Match 94.4%; Score 2950; DB 15; Length 977;
Best Local Similarity 98.4%; Pred. No. 1e-219;
Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYHR 60
DB 1 MLLWVILLVAPVSGQFARTPRPIIFLOPPWTTVFOGERVTLTCKGFRFYSPOKTKWYHR 60
QY 61 YLKGKILRETPDNILEVQESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120
DB 61 YLKGKILRETPDNILEVQESGEYRCQAGSPVHLDFSSASLILQAPLSVPEGDSVV 120
QY 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
DB 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFHACLKONGAYRCTGYKESCCPVSSNT 180
QY 181 VKIQVOEPFTRPVLASSQFISGNBPVTLTCTQLSLERSDVPRLFRFRDDQTLGLWS 240
DB 181 VKIQVOEPFTRPVLASSQFISGNBPVTLTCTQLSLERSDVPRLFRFRDDQTLGLWS 240
QY 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIQVQIPASHPVLTLSPEKALNFE 300
DB 241 LSPNFQITAMWSKDSGFYWCKAATMPHSVIDSPPRSWIQVQIPASHPVLTLSPEKALNFE 300
QY 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
DB 301 GTKVTLHCETQEDSLRTLRYFHEGVPLRHKSVCRCERGASISFSLTENSNGNYCTADNG 360
QY 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQKGSPLIYQFHEDAA 420
DB 361 LGAKPSKAVSLSVTPVSHPVNLSSPEDLIFEGAKVTLHCEAQKGSPLIYQFHEDAA 420
QY 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480
DB 421 LERRSANSAGGVAISFSLTAHSGNYYCTADNGFGQPSKAVSLSVTPVSHPVLTLSA 480
QY 481 EALTTEGATVTLHCEVQSGSPQILYQFYHEDMPLVSSSTPSVGRVSFSLTEGHSNYY 540

Db 541 CTADNGFGPQSEVVSLFVT-----VPVSRPIL 568

Search completed: November 30, 2004, 11:54:25
Job time : 146 secs

Db 481 EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLSSSTPSVGRVSPFSLSLTHSGNYY 540

Qy 541 CTADNGFGPQSEVVSLFVTGCKWVLASKPPL 572

Db 541 CTADNGFGPQSEVVSLFVT-----VPVSRPIL 568

RESULT 15

US-10-403-847-9

; Sequence 9, Application US/10403847

; Publication No. US20040030098A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICED VARIANTS OF A HUMAN

; TITLE OF INVENTION: CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS, BGSSG AND BGSSH

; FILE REFERENCE: D0228 NP

; CURRENT APPLICATION NUMBER: US/10/403,847

; CURRENT FILING DATE: 2003-03-28

; PRIOR APPLICATION NUMBER: U.S. 60/369,671

; PRIOR FILING DATE: 2002-03-29

; PRIOR APPLICATION NUMBER: U.S. 60/371,420

; PRIOR FILING DATE: 2002-04-10

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 9

; LENGTH: 977

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-403-847-9

Query Match 94.4%; Score 2950; DB 15; Length 977;

Best Local Similarity 98.4%; Pred. No. le-219;

Matches 563; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

Qy 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTCKGFRFYSPQTKWYHR 60

Db 1 MLLWVILLVLPVSGQFARTPRPIIFLOPPWTTVFQGERVTLTCKGFRFYSPQTKWYHR 60

Qy 61 YLGEILRETDPNILEVOESGEYECQAGSPLSPVHLDPFSSASLILQAPLSVFGDSVV 120

Db 61 YLGEILRETDPNILEVOESGEYECQAGSPLSPVHLDPFSSASLILQAPLSVFGDSVV 120

Qy 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCYKESCCPVSSNT 180

Db 121 LRCRAKAEVTLNNTIYKNDNVLAFLNKRTPHIFACLKONGAYRCYKESCCPVSSNT 180

Qy 181 VKIQVQEPFTRPVLRASSFPISGNVTLTCTOLSLESDVPLRFRFRDDDTLGLGWS 240

Db 181 VKIQVQEPFTRPVLRASSFPISGNVTLTCTOLSLESDVPLRFRFRDDDTLGLGWS 240

Qy 241 LSPNFQITAMWSKDSGFYWKCAATMPHSVSDSPRSWIOQIPASHPVLTLSPEKALNFE 300

Db 241 LSPNFQITAMWSKDSGFYWKCAATMPHSVSDSPRSWIOQIPASHPVLTLSPEKALNFE 300

Qy 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360

Db 301 GTKVTLHCETQEDSLRTLYRFYHGVPLRHKSVCRCGASISFSLTTENSNGNYCTADNG 360

Qy 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420

Db 361 LGAKPSKAVSLSVTPVSHVPLNLSSPEDLIFEGAKVTLHCEAQRGSLPILYOFHHEDAA 420

Qy 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITVPVSHPVLTLSA 480

Db 421 LERSANSAGGVAISFSLTAHSGNYYCTADNGFGPQSKAVSLSIITVPVSHPVLTLSA 480

Qy 481 EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLSSSTPSVGRVSPFSLSLTHSGNYY 540

Db 481 EALTFEGATVTLHCEVQSGPQILYQFYHEDMPLSSSTPSVGRVSPFSLSLTHSGNYY 540

Qy 541 CTADNGFGPQSEVVSLFVTGCKWVLASKPPL 572